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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 75.4483 Seconds
(without alignments)
520,498 Million cell updates/sec

Title: US-10-007-255-9

Sequence: 1 ctatcagacagcgtcttcaag 24

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	568	2	US-08-439-814-4
2	24	100.0	1318	2	US-08-439-814-3
3	24	100.0	1688	2	US-08-439-814-2
4	24	100.0	2090	2	US-08-439-814-1
5	17.2	71.7	601	4	US-09-949-016-70889
6	17.2	71.7	601	4	US-09-949-016-70890
7	17.2	71.7	13204	4	US-09-054-227-49
8	17.2	71.7	125536	4	US-09-949-016-14186
9	17.2	71.7	276687	4	US-09-949-016-13840
10	17	70.8	92	4	US-09-621-976-17501
11	17	70.8	103	4	US-09-621-976-17501
12	17	70.8	126	4	US-09-621-976-17503
13	17	70.8	137	4	US-09-621-976-17502
14	17	70.8	150	4	US-09-621-976-13989
15	17	70.8	169	4	US-09-621-976-11249
16	17	70.8	179	4	US-09-621-976-9575
17	16.8	70.0	26313	4	US-09-949-016-16117
18	16.8	70.0	81384	4	US-09-949-016-12422
19	16.6	69.2	406	4	US-09-949-016-14718
20	16.6	69.2	601	4	US-09-949-016-29459
21	16.6	69.2	601	4	US-09-949-016-15385
22	16.6	69.2	601	4	US-09-949-016-18573
23	16.6	69.2	601	4	US-09-949-016-195083
24	16.6	69.2	601	4	US-09-949-016-195084
25	16.6	69.2	1572	4	US-09-107-5332A-495
26	16.6	69.2	24847	4	US-09-949-016-16056
27	16.6	69.2	25464	4	US-09-326-480A-4

28	16.6	69.2	28696	4	US-09-949-016-17054	Sequence 17054, A
29	16.6	69.2	28780	4	US-09-949-016-12335	Sequence 12335, A
30	16.6	69.2	40130	4	US-09-949-016-17275	Sequence 17275, A
31	16.6	69.2	142504	4	US-09-949-016-13693	Sequence 13693, A
32	16.6	69.2	142506	4	US-09-949-016-12474	Sequence 12474, A
33	16.6	69.2	248968	4	US-09-949-016-12614	Sequence 12614, A
34	16.6	69.2	250958	4	US-09-949-016-16061	Sequence 16061, A
35	16.6	69.2	260266	4	US-09-949-016-17037	Sequence 17037, A
36	16.6	69.2	260293	4	US-09-949-016-12106	Sequence 12106, A
37	16.6	69.2	1330121	4	US-09-557-884-1	Sequence 1, Appl
38	16.6	69.2	1330121	4	US-09-643-990A-1	Sequence 1, Appl
39	16.2	67.5	856	4	US-09-308-080-7	Sequence 7, Appl
40	16.2	67.5	861	4	US-09-308-080-1	Sequence 1, Appl
41	16.2	67.5	1503	4	US-09-184-418C-29	Sequence 29, Appl
42	16.2	67.5	8953	4	US-09-184-418C-3	Sequence 3, Appl
43	16.2	67.5	41755	4	US-09-949-016-15728	Sequence 15728, A
44	16.2	67.5	200663	4	US-09-949-016-12569	Sequence 12569, A
45	16.2	67.5	203093	4	US-09-949-016-14445	Sequence 14445, A

ALIGNMENTS

RESULT 1
US-08-439-814-4/c
Sequence 4, Application US/08439814
Patent No. 5868735
GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARNELESTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
STREET: Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439, 814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE93/01086

FILED DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-439-814-4

Query Match 100.0%; Score 24; DB 2; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTTTCAAG 24
DB 203 CTTATGTAGACAGCTTTCAAG 180

RESULT 2
US-08-439-814-3/c
Sequence 3, Application US/08439814
Patent No. 5968735
GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
CLASSIFICATION: 514
FILING DATE: 12-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1318 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-439-814-3

Query Match 100.0%; Score 24; DB 2; Length 1318;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTTTCAAG 24
DB 953 CTTATGTAGACAGCTTTCAAG 930

RESULT 3
US-08-439-814-2/c
Sequence 2, Application US/08439814
Patent No. 5968735
GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
CLASSIFICATION: 514
FILING DATE: 12-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1688 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-439-814-2

Query Match 100.0%; Score 24; DB 2; Length 1688;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACAGCTTTTCAAG 24
Db 1323 CTTATGTAGACAGCTTTTCAAG 1300

RESULT 4

US-08-439-814-1/C
Sequence 1, Application US/08439814

Patent No. 5968735

GENERAL INFORMATION:

APPLICANT: STEIN, Ulrike

TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF

TITLE OF INVENTION: THERAPY-RELEVANT GENES

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESS: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP

STREET: 655 Fifteenth Street, N. W., Suite 330 G

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/439, 814

FILING DATE: 12-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 4238778.7

FILING DATE: 12-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE PCT/DE93/01086

FILING DATE: 10-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: KLESNER, Sharon N.

REGISTRATION NUMBER: 36,335

REFERENCE/DOCKET NUMBER: P1614-5015

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P4238778.7

FILING DATE: 12-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/DE93/01086

FILING DATE: 10-NOV-1993

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2090 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-439-814-1

Query Match 100.0%; Score 24; DB 2; Length 2090;
Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACAGCTTTTCAAG 24
Db 1725 CTTATGTAGACAGCTTTTCAAG 1702

RESULT 5

US-09-949-016-70889/C
Sequence 70889, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 70889

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-70889

Query Match 71.7%; Score 17.2; DB 4; Length 601;
Best Local Similarity 86.4%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTATGTAGACAGCTTTTCAAA 23
Db 315 TTATGTATACATGCTTTTAA 294

RESULT 6

US-09-949-016-70890/C
Sequence 70890, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 70890

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-70890

Query Match 71.7%; Score 17.2; DB 4; Length 601;
Best Local Similarity 86.4%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TTATGTAGACAGCTTTTCAAA 23
Db 95 TTATGTATACATGCTTTTAA 74

RESULT 7
US-09-054-272-49
Sequence 49, Application US/09054272
Patent No. 6692909
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Daley, George O.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Rozen, Steven G.
TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,272
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI98-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 13204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-09-054-272-49

Query Match 71.7%; Score 17.2; DB 4; Length 13204;
Best Local Similarity 86.4%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTTTTCAA 22
DB 4230 CTAATGTAGACAGCTTTTCAA 4251

RESULT 8
US-09-949-016-14186/c
Sequence 14186, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14186
LENGTH: 125536
TYPE: DNA
ORGANISM: Human
US-09-949-016-14186

Query Match 71.7%; Score 17.2; DB 4; Length 125536;
Best Local Similarity 86.4%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACAGCTTTTCAA 23
DB 120935 TTATGAAGACAGCTTTTAA 120914

RESULT 9
US-09-949-016-13840/c
Sequence 13840, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13840
LENGTH: 276687
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(276687)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13840

Query Match 71.7%; Score 17.2; DB 4; Length 276687;
Best Local Similarity 86.4%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACAGCTTTTCAA 23
DB 43890 TTATGTATACATGCTTTTAA 43869

RESULT 10
US-09-621-976-17500/c
Sequence 17500, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 17500
LENGTH: 92
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17500

Query Match
Best Local Similarity 100.0%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17
|||||
DB 74 CTTATGTAGACAGCTCT 58

RESULT 11
US-09-621-976-17501/c
Sequence 17501, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 17501
LENGTH: 103
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17501

Query Match
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17
|||||
DB 74 CTTATGTAGACAGCTCT 58

RESULT 12
US-09-621-976-17503/c
Sequence 17503, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 17503
LENGTH: 126
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17503

Query Match
Best Local Similarity 100.0%; Pred. No. 59;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17
|||||
DB 74 CTTATGTAGACAGCTCT 58

RESULT 13
US-09-621-976-17502/c
Sequence 17502, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 17502
LENGTH: 137
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17502

Query Match
Best Local Similarity 100.0%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17
|||||
DB 74 CTTATGTAGACAGCTCT 58

RESULT 14
US-09-621-976-13989/c
Sequence 13989, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 13989
LENGTH: 150
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-13989

Query Match
Best Local Similarity 100.0%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTCT 17
|||||
DB 74 CTTATGTAGACAGCTCT 58

RESULT 15
US-09-621-976-11249/c
Sequence 11249, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm

SEQ ID NO 11249

/ LENGTH: 169
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc_feature
 / LOCATION: 169
 / OTHER INFORMATION: n=a, 5, c or t
 US-09-621-976-11249

Query Match 70.8%; Score 17; DB 4; Length 169;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGTCT 17
 |||||
 Db 74 CTTATGTAGACACGTCT 58

Search completed: February 9, 2005, 17:11:13
 Job time : 79.4483 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 256 Seconds
(without alignments)
539.601 Million cell updates/sec

Title: US-10-007-255-9

Perfect score: 24
Sequence: 1 cttatgtagacacgctttcaag 24

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 431806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA: *
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4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09A_NEW_PUB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	633	18	US-10-482-433A-3
2	24	100.0	2932	18	US-10-473-126-37
3	19.8	82.5	633	18	US-10-482-433A-6
4	19.8	82.5	2932	17	US-10-451-646-24
5	19.8	82.5	2932	18	US-10-473-126-167
6	18.2	75.8	491	18	US-10-437-963-86300
7	18.2	75.8	494	10	US-09-770-961-577
8	18.2	75.8	520	18	US-10-357-930-19155
9	18.2	75.8	597	18	US-10-357-930-54995
10	18.2	75.8	642	18	US-10-357-930-48960
11	18.2	75.8	1504	18	US-10-437-963-86301

12	18.2	75.8	2932	18	US-10-473-126-168	Sequence 168, App
13	18.2	75.8	2932	18	US-10-473-126-313	Sequence 313, App
14	17.8	74.2	619	13	US-10-027-633-8632	Sequence 8632, Ap
15	17.8	74.2	619	17	US-10-027-633-8632	Sequence 8632, Ap
16	17.8	74.2	665	13	US-10-027-633-99405	Sequence 99405, A
17	17.8	74.2	665	13	US-10-027-633-99406	Sequence 99406, A
18	17.8	74.2	665	17	US-10-027-633-99405	Sequence 99405, A
19	17.8	74.2	665	17	US-10-027-633-99406	Sequence 99406, A
20	17.8	74.2	665	17	US-10-027-633-99406	Sequence 99406, A
21	17.8	74.2	303172	18	US-10-719-993-6890	Sequence 6890, Ap
22	17.6	73.3	277	10	US-09-814-353-12011	Sequence 12011, A
23	17.6	73.3	340	18	US-10-357-930-50147	Sequence 50147, A
24	17.6	73.3	1353	18	US-10-282-122A-38309	Sequence 38309, A
25	17.4	72.5	201	18	US-10-741-601-19969	Sequence 19969, A
26	17.4	72.5	61177	18	US-10-741-601-55694	Sequence 55694, Ap
27	17.2	71.7	25	15	US-10-098-263B-4459	Sequence 4459, A
28	17.2	71.7	159	15	US-10-097-111-147	Sequence 147, App
29	17.2	71.7	392	18	US-10-674-124A-13252	Sequence 13252, A
30	17.2	71.7	633	13	US-10-027-633-274931	Sequence 274931, A
31	17.2	71.7	633	13	US-10-027-633-274932	Sequence 274932, A
32	17.2	71.7	633	17	US-10-027-633-274932	Sequence 274932, A
33	17.2	71.7	633	17	US-10-027-633-274932	Sequence 274932, A
34	17.2	71.7	780	18	US-10-437-963-23635	Sequence 23635, A
35	17.2	71.7	840	15	US-10-425-114-10735	Sequence 10735, A
36	17.2	71.7	869	17	US-10-425-114-10735	Sequence 18304, A
37	17.2	71.7	1067	17	US-10-424-599-35770	Sequence 700, App
38	17.2	71.7	1446	17	US-10-424-599-35770	Sequence 18304, A
39	17.2	71.7	15783	10	US-09-764-872-700	Sequence 6811, Ap
40	17.2	71.7	28953	18	US-10-719-993-6811	Sequence 6811, Ap
41	17.2	71.7	56506	15	US-10-097-111-10	Sequence 10735, A
42	17.2	70.8	342	9	US-09-864-761-6452	Sequence 6452, Ap
43	16.8	70.0	635	13	US-10-637-855-398	Sequence 398, App
44	16.8	70.0	635	13	US-10-027-632-214760	Sequence 214760, A
45	16.8	70.0	635	13	US-10-027-632-214761	Sequence 214761, A

ALIGNMENTS

RESULT 1
US-10-482-433A-3/c
; Sequence 3, Application US/10482433A
; Publication No. US20040265814A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method for the detection of cytosine methylation by comparative
; FILE REFERENCE: 82174
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: DE 10132212.7
; PRIORITY FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amplification Product of MdRI-Fragment
US-10-482-433A-3

Query Match 100.0%; Score 24; DB 18; Length 633;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTCAAG 24
|||||
DB 211 CTTATGTAGACACGCTTTCAAG 188
|||||

RESULT 2
US-10-473-126-37/c

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Sequence 37, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 37
LENGTH: 2932
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-473-126-37
```

```
Query Match
Best Local Similarity 100.0%; Score 24; DB 18; Length 2932;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 CTTATGTAGACACGCTCTTCAAA 24
DB 828 CTTATGTAGACACGCTCTTCAAG 805
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```
RESULT 3
US-10-482-433A-6/c
Sequence 6, Application US/10482433A
Publication No. US20040265814A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method for the detection of cytosine methylation by comparative
FILE REFERENCE: 82174
CURRENT APPLICATION NUMBER: US/10/482,433A
CURRENT FILING DATE: 2003-12-29
PRIOR APPLICATION NUMBER: DE 10132212.7
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 633
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Amplification Product Of Bisulfite-Treated DNA
US-10-482-433A-6
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```
Query Match
Best Local Similarity 82.5%; Score 19.8; DB 18; Length 633;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 CTTATGTAGACACGCTCTTCAAA 23
DB 211 CTTATATATAACACGCTCTTCAAA 189
```

```
RESULT 4
US-10-451-646-24/c
Sequence 24, Application US/10451646
Publication No. US20040067508A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method for the Simultaneous Amplification of Multiple
FILE REFERENCE: PCT/DE 01/04951
CURRENT APPLICATION NUMBER: US/10/451,646
CURRENT FILING DATE: 2003-06-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 2932
TYPE: DNA
```

```
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: bisulphite treated sequence
US-10-451-646-24
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```
Query Match
Best Local Similarity 82.5%; Score 19.8; DB 17; Length 2932;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 CTTATGTAGACACGCTCTTCAAA 23
DB 828 CTTATATATAACACGCTCTTCAAA 806
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```
RESULT 5
US-10-473-126-167/c
Sequence 167, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 167
LENGTH: 2932
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-167
```

```
Query Match
Best Local Similarity 82.5%; Score 19.8; DB 18; Length 2932;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CTTATGTAGACACGCTCTTCAAA 23
DB 828 CTTATATATAACACGCTCTTCAAA 806
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```
RESULT 6
US-10-437-963-86300
Sequence 86300, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 86300
LENGTH: 491
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(491)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_85354C.1
US-10-437-963-86300
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Query Match 75.8%; Score 18.2; DB 18; Length 494;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTATGTAGACAGCTTTCAAG 24
DB 53 TTATGTAGACAGCTTTCAAG 75

RESULT 7

US-09-770-961-577/C
Sequence 577, Application US/09770961
Publication No. US20030115639A1
GENERAL INFORMATION:
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameake, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moesner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thalians
FILE REFERENCE: 2026 (PARA-015PRV)
CURRENT APPLICATION NUMBER: US/09/770.961
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,466
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 577
LENGTH: 494
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-961-577

Query Match 75.8%; Score 18.2; DB 10; Length 494;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TTATGTAGACAGCTTTCAAG 24
DB 297 TTATGTAGACAGCTTTCAAG 275

RESULT 8

US-10-357-930-19156
Sequence 19156, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276

PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19156
LENGTH: 520
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 166..171
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-19156

Query Match 75.8%; Score 18.2; DB 18; Length 520;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CTTATGTAGACAGCTTTCAAA 23
DB 303 CTTATGTAGACAGCTTTCAAA 325

RESULT 9

US-10-357-930-54995/C
Sequence 54995, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54995
LENGTH: 597
TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-54995

Query Match 75.8%; Score 18.2; DB 18; Length 597;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTTTTCAA 23
|||
Db 142 CTTATGTAGATATGCTTTCAA 120

RESULT 10
US-10-357-930-48960
; Sequence 48960, Application US/10357930
; Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert
APPLICANT: Endeguel, Wilson
APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357,930

PRIOR FILING DATE: 2003-02-04

PRIOR FILING DATE: 2003-02-16

PRIOR FILING DATE: 2003-02-16

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR FILING DATE: 2000-03-16

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255,281

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 48960

LENGTH: 642

TYPE: DNA

ORGANISM: Homo sapiens

US-10-357-930-48960

Query Match

Best Local Similarity 75.8%; Score 18.2; DB 18; Length 642;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTTTTCAA 23

|||

Db 372 CTTATGTAGACTCTTTTCAA 394

RESULT 11

US-10-437-963-86301

; Sequence 86301, Application US/10437963

; Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovacic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Bouharov, Andrey A.

APPLICANT: Barbazuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_86355C.1
US-10-437-963-86301

Query Match
Best Local Similarity 75.8%; Score 18.2; DB 18; Length 1504;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACAGCTTTTCAAAG 24

|||

Db 189 TTATGTAGATATGCTTTCAAAG 211

RESULT 12

US-10-473-126-168

; Sequence 168, Application US/10473126

; Publication No. US20040234973A1

GENERAL INFORMATION:

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/473,126

PRIOR FILING DATE: 2003-09-26

NUMBER OF SEQ ID NOS: 1258

SEQ ID NO 168

LENGTH: 2932

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-473-126-168

Query Match

Best Local Similarity 75.8%; Score 18.2; DB 18; Length 2932;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACAGCTTTTCAAAG 24

|||

Db 2106 TTATGTAGATATGCTTTTCAAAG 2128

RESULT 13

US-10-473-126-313/C

; Sequence 313, Application US/10473126

; Publication No. US20040234973A1

GENERAL INFORMATION:

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/473,126

PRIOR FILING DATE: 2003-09-26

NUMBER OF SEQ ID NOS: 1258

SEQ ID NO 313

LENGTH: 2932

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-473-126-313

Query Match

Best Local Similarity 75.8%; Score 18.2; DB 18; Length 2932;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACAGCTTTTCAA 23

|||

Db 828 CTTATGTATTAACATCTTTCAA 806

RESULT 14

```

US-10-027-632-8632
; Sequence 8632, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8632
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-8632

```

```

Query Match          74.2%; Score 17.8; DB 13; Length 619;
Best Local Similarity 90.5%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      3 TATGTAGACAGCTTTTCAA 23
      ||| ||||| ||||| |||||
Db      523 TATGAAGACAGCTTTTCAA 543

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RESULT 15
US-10-027-632-8632
; Sequence 8632, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8632
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-8632

```

```

Query Match          74.2%; Score 17.8; DB 17; Length 619;
Best Local Similarity 90.5%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      3 TATGTAGACAGCTTTTCAA 23
      ||| ||||| ||||| |||||
Db      523 TATGAAGACAGCTTTTCAA 543

```

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Search completed: February 9, 2005, 22:26:35
Job time : 257 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 235.862 Seconds
(without alignments)
602.360 Million cell updates/sec

Title: US-10-007-255-9
Perfect score: 24
Sequence: 1 ctatcgtacacgacgtcttcaag 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseq19808:*
2: geneseq19908:*
3: geneseq20008:*
4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	24	6 AAD39008	Aad39008 Human mdr
C 2	24	100.0	24	6 AAD38998	Aad38998 Human mdr
C 3	24	100.0	568	2 AAG62615	Aag62615 Human mdr
C 4	24	100.0	633	8 ABX94595	Abx94595 Human mdr
C 5	24	100.0	1318	2 AAG62614	Aag62614 Human mdr
C 6	24	100.0	1688	2 AAG62613	Aag62613 Human mdr
C 7	24	100.0	2090	2 AAG62612	Aag62612 Human mdr
C 8	24	100.0	2932	10 ABE20987	Ab20987 Human 5'
C 9	24	100.0	2932	10 ADE53945	Ad53945 MDR1 geno
C 10	24	100.0	2932	10 ADE84005	Ad84005 5' regula
C 11	24	100.0	2932	13 ADS88985	Ad88985 Human ABC
C 12	24	100.0	8573	6 ABS98184	Ab98184 Human mul
C 13	24	100.0	10200	6 AAD41243	Aad41243 Human mdr
C 14	24	100.0	177380	8 ACF62751	Ac62751 Cancer ba
C 15	24	100.0	177380	8 ADB20870	Ad20870 MRP1 base
C 16	24	100.0	177380	10 ADB87959	Ad87959 Human UGT
C 17	24	100.0	177380	10 ADB96942	Ad96942 Human MDR
C 18	24	100.0	177380	10 ADB92133	Ad92133 Human mdr
C 19	23	95.8	23	6 AAD39037	Aad39037 Human mdr
C 20	23	95.8	23	6 AAD39033	Aad39033 Human mdr

C 21	22	91.7	22	6 AAD39034	Aad39034 Human mdr
C 22	22	91.7	22	6 AAD39038	Aad39038 Human mdr
C 23	21	87.5	21	6 AAD39035	Aad39035 Human mdr
C 24	21	87.5	21	6 AAD39039	Aad39039 Human mdr
C 25	20	83.3	20	6 AAD39040	Aad39040 Human mdr
C 26	19.8	82.5	633	8 ABX94598	Abx94598 Human mdr
C 27	19.8	82.5	2932	6 ABN85526	Abn85526 Human b1s
C 28	19.8	82.5	2932	8 AB210027	Ab210027 Haematopo
C 29	19.8	82.5	2932	10 ADB54077	Ad54077 Pretreate
C 30	19.8	82.5	2932	10 ADB84065	Ad84065 Human lym
C 31	19.8	82.5	2932	13 ADS89231	Ad89231 Oligonuc1
C 32	19	79.2	19	4 AAF91153	Aaf91153 Human mul
C 33	19	79.2	19	4 AAF91155	Aaf91155 Human mul
C 34	18.8	78.3	650	4 AAF88286	Aaf88286 H. tuberc
C 35	18.6	77.5	19	4 AAF91154	Aaf91154 Human mul
C 36	18.6	77.5	19	4 AAF91156	Aaf91156 Human mul
C 37	18.6	77.5	19	8 ACF62678	Ac62678 Cancer ba
C 38	18.6	77.5	19	8 ACF62678	Ac62678 Cancer ba
C 39	18.6	77.5	19	8 ADB21349	Ad21349 MRP1 base
C 40	18.6	77.5	19	8 ADB21350	Ad21350 MRP1 base
C 41	18.6	77.5	19	10 ADB88438	Ad88438 Human UGT
C 42	18.6	77.5	19	10 ADB88439	Ad88439 Human UGT
C 43	18.6	77.5	19	10 ADB87421	Ad87421 Human MDR
C 44	18.6	77.5	19	10 ADB97422	Ad97422 Human MDR
C 45	18.6	77.5	19	10 ADB92613	Ad92613 Human MDR

ALIGNMENTS

RESULT 1	AAD39008/c	AAD39008 standard; DNA; 24 BP.
ID	AAD39008	
XX		
AC	AAD39008;	
XX		
DT	23-SEP-2002	(first entry)
XX		
DE	Human mdr1 gene HIF-1 binding site DNA #1.	
XX		
XX	Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;	
KW	hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;	
KW	lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;	
KW	myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;	
KW	angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;	
KW	polycythaemia vera; hypoxia responsive element; HRE; ds.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	misc_binding	10..14
FT		/*tag= a
FT		/bound_molecly= "HIF-1"
XX		
PN	WO200234291-A2.	
XX		
PD	02-MAY-2002.	
XX		
XX	25-OCT-2001; 2001WO-US049856.	
XX		
PR	26-OCT-2000; 2000US-0243542P.	
XX		
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.	
XX		
PI	Colgan SP;	
XX		
DR	WPI; 2002-471427/50.	
XX		
PT	Treating a subject (at risk of) having a hematologic malignancy or	
PT	multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia	
PT	inducible factor 1 binding molecules or small ubiquitin-like-modifier-1	
PT	binding molecules.	
XX		

PS Example 2; Page 12; 92pp; English.
XX
CC The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphocytic leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is human mdr1
CC gene HIF-1 binding site DNA
SQ
Sequence 24 BP; 8 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 24 CTTATGTAGACACGCTTTCAAG 1
RESULT 2
AAD38998
ID AAD38998 standard; DNA; 24 BP.
XX
AC AAD38998;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human mdr1-HRE antisense oligonucleotide #1.
XX
KW Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;
KW hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;
KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
KW myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;
KW angiotenic myeloid metaplasia; myeloid leukaemia; gene therapy;
KW polycythaemia vera; hypoxia responsive element; HRE; antisense;
KW phosphorothioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..24 /*tag= a
FT modified_base 1..24 /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PN W0200234291-A2.
XX
PD 02-MAY-2002.
XX
PF 25-OCT-2001; 2001WO-US049856.
XX
PR 26-OCT-2000; 2000US-0243542P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Colgan SP;
XX
WI WPI; 2002-471427/50.
XX
PT Treating a subject (at risk of) having a hematologic malignancy or
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia
PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

PT binding molecules.
XX
PS Claim 14; Page 43; 92pp; English.
XX
CC The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphocytic leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is an antisense
CC oligo targeted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its
CC expression. This oligo is used in the exemplification of the invention
SQ
Sequence 24 BP; 7 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 1 CTTATGTAGACACGCTTTCAAG 24
RESULT 3
AAQ62615/c
ID AAQ62615 standard; DNA; 568 BP.
XX
AC AAQ62615;
XX
DT 25-MAR-2003 (revised)
DT 17-JAN-1995 (first entry)
XX
DE Human mdr-1 promoter fragment.
XX
KW Inducible promoter; cytostatic agent; adriamycin; vincristine;
KW multiple drug resistance; mdr-1; mammalian expression vector;
KW cancer therapy; ss.
XX
OS Homo sapiens.
OS
PN DE4238778-A1.
PN 19-MAY-1994.
PD
PF 12-NOV-1992; 92DE-04238778.
XX
PR 12-NOV-1992; 92DE-04238778.
XX
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Stein U, Walthers W;
XX
WI WPI; 1994-168680/21.
XX
PT New mammalian expression vector useful for gene therapy, - comprising the
PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to
PT cytostatic agents.
XX
PS Claim 2; Page 6; 7pp; German.
XX
CC This is a preferred fragment of the mdr-1 gene promoter, isolated from
CC human DNA. The mdr-1 promoter and enhancer elements are inducible by
CC cytostatic agents such as vincristine and adriamycin which are used in
CC cancer therapy. Vectors comprising the promoter and enhancer sequences

CC operably linked to heterologous genes coding for therapeutic agents are
 CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
 CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
 CC control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 SQ Sequence 568 BP; 142 A; 127 C; 143 G; 156 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 2; Length 568;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CTTATGTAGACACGCTTTCAAG 24
 Db 203 CTTATGTAGACACGCTTTCAAG 180
 RESULT 4
 ABX94595/c
 ID ABX94595 standard; DNA; 633 BP.
 AC
 XX ABX94595;
 XX
 DT 17-JUN-2003 (first entry)
 DE Human Mdr1 DNA SEQ ID 3.
 XX
 XX Mdr1; cytosine methylation; hydrogen sulphite; diagnose; dementia;
 XX 5-methylcytosine; amplification; prognosis; side effect; medication; bone;
 XX cancer; central nervous system disorder; aggression; muscle; endocrine;
 XX abnormal development; personality disorder; behavioural disorder; injury;
 XX brain damage; psychotic disorder; cardiovascular disease; infection;
 XX gastrointestinal tract; sexual malfunction; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003002760-A2.
 XX
 PD 09-JAN-2003.
 XX
 PE 27-JUN-2002; 2002MO-DE002433.
 XX
 PR 27-JUN-2001; 2001DE-01032212.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Dietler J, Leu E;
 XX
 PS WPI; 2003-201513/19.
 DR
 XX
 XX Determining cytosine methylation in a genomic DNA sample by treating with
 PT hydrogen sulfitte and analyzing the result, to diagnose associated
 PT conditions including cancer and brain disorders.
 PS
 XX Example 1; Page 17; 38pp; German.
 CC
 CC This invention describes a novel method of determining cytosine
 CC methylation in a sample of genomic DNA which comprises treating the
 CC sample with hydrogen sulphite so that the cytosine is converted to uracil
 CC whilst 5-methylcytosine remains unchanged, amplifying sections of both
 CC using at least 2 PCR primers and studying the base composition of both
 CC complementary amplified strands whereby methylation status is deduced
 CC from the difference in molecular weight of the two strands. The method is
 CC used to diagnose and/or prognosis unwanted side effects of medication,
 CC cancer, central nervous system disorders, aggression symptoms or
 CC behavioural disorders, clinical, psychological and social consequence of
 CC brain damage, psychotic and personality disorders, dementia and
 CC associated disorders, cardiovascular disease, malfunction, damage or
 CC disease of the gastrointestinal tract, breathing system, bone muscle,
 CC endocrine or metabolic system, injury, infection, abnormal development or
 CC sexual malfunction. This sequence represents the human Mdr1 DNA fragment
 CC amplified by the PCR primers represented in ABX94593 & ABX94594 and is
 CC used to illustrate the method of the invention

XX
 SQ Sequence 633 BP; 161 A; 143 C; 165 G; 164 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 8; Length 633;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CTTATGTAGACACGCTTTCAAG 24
 Db 211 CTTATGTAGACACGCTTTCAAG 188
 RESULT 5
 AAQ62614/c
 ID AAQ62614 standard; DNA; 1318 BP.
 AC
 XX AAQ62614;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-JAN-1995 (first entry)
 XX
 DE Human mdr-1 promoter fragment.
 XX
 XX inducible promoter; cytostatic agent; adriamycin; vincristine;
 XX multiple drug resistance; mdr-1; mammalian expression vector;
 XX cancer therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE4238778-A1.
 XX
 PD 19-MAY-1994.
 XX
 PE 12-NOV-1992; 92DE-04238778.
 XX
 PR 12-NOV-1992; 92DE-04238778.
 XX
 PA (DELB-) DELBUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 PI Stein U, Walthert W;
 XX
 PS WPI; 1994-168680/21.
 DR
 XX
 XX New mammalian expression vector useful for gene therapy, - comprising the
 PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to
 PT cytostatic agents.
 PS
 XX Claim 2; Page 5; 7pp; German.
 CC
 CC This is a preferred fragment of the mdr-1 gene promoter, isolated from
 CC human DNA. The mdr-1 promoter and enhancer elements are inducible by
 CC cytostatic agents such as vincristine and adriamycin which are used in
 CC cancer therapy. Vectors comprising the promoter and enhancer sequences
 CC operably linked to heterologous genes coding for therapeutic agents are
 CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
 CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
 CC control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 SQ Sequence 1318 BP; 430 A; 237 C; 277 G; 374 T; 0 U; 0 Other;
 Query Match 100.0%; Score 24; DB 2; Length 1318;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CTTATGTAGACACGCTTTCAAG 24
 Db 953 CTTATGTAGACACGCTTTCAAG 930
 RESULT 6
 AAQ62613/c
 ID AAQ62613 standard; DNA; 1688 BP.

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XX AC AA062613;
XX XX 25-MAR-2003 (revised)
DT 17-JAN-1995 (first entry)
XX XX Human mdr-1 promoter fragment.
DE XX
XX KW inducible promoter; cytosstatic agent; adriamycin; vincristine;
KW multiple drug resistance; mdr-1; mammalian expression vector;
KW cancer therapy; ss.
XX OS Homo sapiens.
XX PN DE4238778-A1.
XX PD 19-MAY-1994.
XX PF 12-NOV-1992; 92DE-04238778.
XX PR 12-NOV-1992; 92DE-04238778.
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Stein U, Walther W;
XX PI WPI; 1994-168680/21.
XX DR
XX CC New mammalian expression vector useful for gene therapy, - comprising the
XX PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to
XX FT cytosstatic agents.
XX PS Claim 2; Page 5; 7pp; German.
XX XX
XX CC This is a preferred fragment of the mdr-1 gene promoter, isolated from
XX CC human DNA. The mdr-1 promoter and enhancer elements are inducible by
XX CC cytosstatic agents such as vincristine and adriamycin which are used in
XX CC cancer therapy. Vectors comprising the promoter and enhancer sequences
XX CC operably linked to heterologous genes coding for therapeutic agents are
XX CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
XX CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
XX CC control of cytosstatic agents. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 1688 BP; 556 A; 311 C; 371 G; 450 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 24; DB 2; Length 1688;
XX Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
XX Matches 24; Conservative 0; Mismatches 0;
QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 1323 CTTATGTAGACACGCTTTCAAG 1300

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XX PD 19-MAY-1994.
XX PF 12-NOV-1992; 92DE-04238778.
XX PR 12-NOV-1992; 92DE-04238778.
XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX PI Stein U, Walther W;
XX PI WPI; 1994-168680/21.
XX DR
XX CC New mammalian expression vector useful for gene therapy, - comprising the
XX PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to
XX FT cytosstatic agents.
XX PS Claim 2; Page 4; 7pp; German.
XX XX
XX CC This is a preferred fragment of the mdr-1 gene promoter, isolated from
XX CC human DNA. The mdr-1 promoter and enhancer elements are inducible by
XX CC cytosstatic agents such as vincristine and adriamycin which are used in
XX CC cancer therapy. Vectors comprising the promoter and enhancer sequences
XX CC operably linked to heterologous genes coding for therapeutic agents are
XX CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
XX CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
XX CC control of cytosstatic agents. (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 2090 BP; 714 A; 365 C; 444 G; 567 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 24; DB 2; Length 2090;
XX Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
XX Matches 24; Conservative 0; Mismatches 0;
QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 1725 CTTATGTAGACACGCTTTCAAG 1702

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RESULT 7
AA062612/c
ID AA062612 standard; DNA; 2090 BP.
XX
XX AA062612;
XX
XX 25-MAR-2003 (revised)
DT 17-JAN-1995 (first entry)
XX
XX Human mdr-1 promoter fragment.
XX
XX KW inducible promoter; cytosstatic agent; adriamycin; vincristine;
KW multiple drug resistance; mdr-1; mammalian expression vector;
KW cancer therapy; ss.
XX OS Homo sapiens.
XX PN DE4238778-A1.

```

```

RESULT 8
ABZ09897/c
ID ABZ09897 standard; DNA; 2932 BP.
XX
XX ABZ09897;
XX
XX 16-JAN-2003 (first entry)
DT
XX
XX Human 5' and/or regulatory region of MDR1 DNA SEQ ID NO:37.
DE
XX
XX Human; haematopoietic cell proliferation disorder; cytosstatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
XX Homo sapiens.
XX OS
XX WO20027272-A2.
XX PN
XX 03-OCT-2002.
XX PD
XX 26-MAR-2002; 2002WO-EP003401.
XX PF
XX 26-MAR-2001; 2001US-0278333P.
XX PR
XX (EPIG-) EPIGENOMICS AG.
XX PA
XX Berlin K, Braun A, Distler J, Gueutig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipschier E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwabe I, Ziebarth H;
XX WPI; 2003-018942/01.
XX DR
XX

```

PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 38; SEQ ID NO 37; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between hematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. AB209861 to AB21118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used for
CC differentiating between healthy hematopoietic cells and proliferative
CC disorder hematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of hematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of hematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC hematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of hematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
SQ Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 8; Length 2932;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTTATGTAGACACGCTTTCAAG 24
DB 828 CTTATGTAGACACGCTTTCAAG 805
RESULT 9
ADBS3945/c
ID ADBS3945 standard; DNA; 2932 BP.
XX
AC ADBS3945;
XX
DT 04-DEC-2003 (first entry)
XX
DE MDRI genomic DNA region.
XX
KW colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytosine; cancer; adenoma; carcinoma; cytosine methylation state; ds.
XX
OS unidentified.
XX
PN WO2003072821-A2.
XX
PD 04-SEP-2003.
XX
PF 27-FEB-2003; 2003WO-EP02035.
XX
PR 27-FEB-2003; 2002EP-0004551.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimrich I, Becker E, Lesche R;
PI Rujan T, Schmitt A;
XX
DR WPI; 2003-731620/69.
XX
PT Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with

PT a reagent.
XX
PS Claim 46; SEQ ID NO 1; 74pp; English.
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytosine methylation activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the genomic DNA region of
CC the invention. This sequence is not shown within the specification but is
CC taken from Wipoweb.
XX
SQ Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 10; Length 2932;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTTATGTAGACACGCTTTCAAG 24
DB 828 CTTATGTAGACACGCTTTCAAG 805
RESULT 10
ADEB4005/c
ID ADEB4005 standard; DNA; 2932 BP.
XX
AC ADEB4005;
XX
DT 29-JAN-2004 (first entry)
XX
DE 5' regulatory region of human gene MDRI.
XX
KW ds; lymphoid cell proliferative disorder; methylation;
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis.
XX
OS Homo sapiens.
XX
PN WO2003044226-A2.
XX
PD 30-MAY-2003.
XX
PF 25-NOV-2002; 2002WO-EP013265.
XX
PR 23-NOV-2001; 2001DE-01057491.
XX
PR 28-DEC-2001; 2001DE-01064501.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimrich I;
PI WPI; 2003-457621/43.
XX
DR WPI; 2003-457621/43.
XX
PT Detecting and differentiating between lymphoid cell proliferative
PT disorders comprises contacting a target nucleic acid with at least one
PT reagent that distinguishes between methylated and non-methylated CpG
PT dinucleotides.
XX
PS Disclosure; SEQ ID NO 1; 446pp; English.
XX
CC The invention relates to a method of detecting and differentiating
CC between lymphoid cell proliferative disorders associated with at least

CC one gene and/or their regulatory regions in a subject by contacting a
 CC target nucleic acid in a biological sample obtained from the subject with
 CC at least one reagent or series of reagents that distinguish between
 CC methylated and non-methylated CpG dinucleotides within the target nucleic
 CC acid. The genes and/or their regulatory regions are preferably selected
 CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPB beta, MYO1, CDH3,
 CC MYC11, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN2A, CDKN2B, FOS,
 CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C,
 CC GSK3beta, ESRR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
 CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
 CC of the genes are useful for detecting the methylation state of all the
 CC CpG dinucleotides within one or more the sequences, or their complements,
 CC for determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs), and for differentiating at least two of the medical
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
 CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
 CC lymphoma. They are also useful for detecting of a predisposition to,
 CC differentiation between subclasses, diagnosis, prognosis, treating and/or
 CC monitoring of lymphoid cell proliferative disorder. This sequence
 CC represents the 5' and/or regulatory region from one of the above
 CC mentioned genes.

CC Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 24; DB 10; Length 2932;
 CC Best Local Similarity 100.0%; Pred. No. 0.15;
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 CTTATGTAGACACGCTTTCAAG 24
 CC |||||
 CC 828 CTTATGTAGACACGCTTTCAAG 805

CC RESULT 11

CC ADS88985/c
 CC ID ADS88985 standard; DNA; 2932 BP.

CC ADS88985;

CC 18-NOV-2004 (first entry)

CC Human ABCB1 gene SEQ ID NO:1.

CC de; gene; human; cell proliferative disorder; breast; methylation;
 CC cytostatic; gene therapy; single nucleotide polymorphism; SNP.

CC Homo sapiens.

CC WO2004035803-A2.

CC 29-APR-2004.

CC 01-OCT-2003; 2003WO-EP010881.

CC 01-OCT-2002; 2002DE-01045779.

CC 07-JAN-2003; 2003DE-01000096.

CC 17-APR-2003; 2003DE-01017955.

CC (EPIC-) EPIGENOMICS AG.

CC Foekeus J, Harbeck N, Koenig T, Majer S, Martens J, Model F,
 CC Nimnich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
 CC WPI; 2004-348468/32.

CC Predicting responsiveness of a subject with breast cell proliferative
 CC disorder, useful for treating or differentiating breast cell
 CC proliferative disorders comprises analyzing methylation pattern of a
 CC genomic DNA from the subject.

CC Example 2; SEQ ID NO 1; 104pp; English.

CC The invention relates to a novel method for predicting the responsiveness

CC of a subject with a cell proliferative disorder of the breast tissues to
 CC a therapy comprising analysing the methylation pattern of a target
 CC nucleic acid by contacting at least one of the target nucleic acids in a
 CC biological sample obtained from the subject prior to or during treatment.
 CC The method of the invention has cytostatic activity, and may have a use
 CC in gene therapy. The set of oligonucleotides comprising at least two of
 CC the oligomers are useful for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The
 CC methods, nucleic acid, oligonucleotide, and kit are useful for the
 CC treatment, characterisation, classification and/or differentiation, of
 CC breast cell proliferative disorders. The method is also useful for
 CC predicting the responsiveness of a subject with a cell proliferative
 CC disorder of the breast tissues to a therapy. The present sequence is used
 CC in the exemplification of the invention.

CC Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 24; DB 13; Length 2932;
 CC Best Local Similarity 100.0%; Pred. No. 0.15;
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 CTTATGTAGACACGCTTTCAAG 24
 CC |||||
 CC 828 CTTATGTAGACACGCTTTCAAG 805

CC RESULT 12

CC ABS98184/c
 CC ID ABS98184 standard; DNA; 8573 BP.

CC ABS98184;

CC 23-DEC-2002 (first entry)

CC Human multidrug resistance gene promoter B and exons 1-3 sequence.

CC Human; de; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1;
 CC cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
 CC adrenergic receptor beta1; ADAR1; aryl hydrocarbon; AHR; MRP3; NR112;
 CC aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 CC cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 CC epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 CC glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 CC HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 CC NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase; thiolabile; STM;
 CC UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 CC UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;
 CC multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 CC multidrug resistance associated protein 3; cancer; prostate;
 CC acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 CC altered drug metabolism; cardiovascular function; colorectal tumour;
 CC central nervous system; pulmonary; immunological; SNP;
 CC single nucleotide polymorphism.

CC Homo sapiens.

CC WO200257410-A2.

CC 25-JUL-2002.

CC 28-NOV-2001; 2001WO-US044838.

CC 28-NOV-2000; 2000US-00724389.

CC (DNAS-) DNA SCI LAB INC.

CC Guida M, Hall J;

CC WPI; 2002-698522/75.

CC Isolated nucleic acid molecules having polymorphisms in known human genes
 CC e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
 CC for locating, identifying and characterizing the genes responsible for

disorder-related traits.

Example 22; Page 432-437; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2), cytochrome P450 02B1 (CYP45002B1), adrenoregic receptor beta1 (ADRB1), aryl hydrocarbon receptor (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), catepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoxidoreductase (SOD), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), uridine kinase receptor (UPA), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502B1, AHR, EPHX2, GST12, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumors, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary, immunological or haematological function, in KRX for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a polymorphic DNA sequence of the invention

Sequence 8573 BP; 2739 A; 1422 C; 1705 G; 2707 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 8573;

Best Local Similarity 100.0%; Pred. No. 0.16; Mismatches 24; Conservative 0; Indels 0; Gaps 0;

1 CTTATGTAGACACGCTTTCAAG 24

1773 CTTATGTAGACACGCTTTCAAG 1750

RESULT 13
AADD1243/C
ID AADD1243 standard; DNA; 10200 BP.

AADD1243;

30-OCT-2002 (first entry)

Human MDR1 gene 5' flanking region.

Human, transgenic; reporter construct; CYP3A4; cytochrome P450;

transcriptional regulatory element; xenobiotic; steroid; MDR1;

p-glycoprotein; gene; ds.

Homo sapiens.

WO200236784-A1.

10-MAY-2002.

01-NOV-2001; 2001WO-AU001407.

01-NOV-2000; 2000AU-00001161.

10-MAY-2001; 2001AU-00004901.

(UNSY) UNIV SYDNEY.

Liddle C, Goodwin BJ, Robertson G;

WPI; 2002-537301/57;

Non-human mammal for determining the effect of a compound on regulation of CYP3A4 gene expression, comprises a reporter construct for producing a reporter linked to a transcriptional regulatory nucleic acid from a human CYP3A4 gene.

Claim 11; Page 83-92; 95pp; English.

The invention relates to generation of non-human transgenic animals comprising a reporter construct for producing a detectable amount of a reporter molecule operably linked to a transcriptional regulatory nucleic acid molecule from the human CYP3A4 gene. The invention also relates to transgenic animal for analysing CYP3A4 cytochrome P450 gene regulation. The non-human mammal of the invention is useful for determining whether a compound is capable of affecting the transcription of a human CYP3A4 gene. It is also useful for determining the effect of a compound such as a xenobiotic or steroid on the regulation of expression of the CYP3A4 gene in a human. The present sequence is 5' flanking region of human (p-glycoprotein) MDR1 gene. This sequence is used as a regulatory element in the invention

Sequence 10200 BP; 3296 A; 1785 C; 1985 G; 3134 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 10200;

Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 24; Conservative 0; Indels 0; Gaps 0;

1 CTTATGTAGACACGCTTTCAAG 24

9051 CTTATGTAGACACGCTTTCAAG 9028

RESULT 14

ACF62751/C

ACF62751 standard; DNA; 177380 BP.

ACF62751;

08-OCT-2003 (first entry)

Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.

Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;

cytochrome p450; subfamily 11A; nifedipine oxidase; polypeptide 5;

cytostatic; gene; ds.

Unidentified.

WO2003013534-A2.

20-FEB-2003.

23-JUL-2002; 2002WO-EP008219.

23-JUL-2001; 2001EP-00117608.

24-MAY-2002; 2002EP-00011710.

(EPID-) EPIDAUDROS BIOTECHNOLOGIE AG.

Heinrich G, Kerb R;

WPI; 2003-268144/26.

PT New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,
PT subfamily I1A, polypeptide 5 polynucleotide, termed CYP3A5.
XX
PS Disclosure; SEQ ID NO 683; 86pp; English.
XX
CC The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily I1A (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACP62200
CC to ACP62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 8; Length 177380;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 140580 CTTATGTAGACACGCTTTCAAG 140557
RESULT 15
ID ADB20870/c ADB20870 standard; DNA; 177380 BP.
XX
AC ADB20870;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:683.
XX
KM irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KM ds.
XX
OS Unidentified.
XX
PN WO2003013533-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002MO-EP008200.
XX
PR 23-JUL-2001; 2001EP-00117608.
XX
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX
DR WPI; 2003-354397/33.
XX
PT Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a
PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.
XX
PS Disclosure; SEQ ID NO 683; 100pp; English.
XX
CC The present invention describes a method for the use of irinotecan (I) or

CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a multidrug resistance protein 1 (MRP1)
CC polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
CC can be used for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject, where the subject is a human
CC (preferably African or Asian) or a mouse. The present sequence represents
CC a sequence which is used in the exemplification of the present invention.
XX
SQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 8; Length 177380;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 140580 CTTATGTAGACACGCTTTCAAG 140557

Search completed: February 9, 2005, 16:05:52
Job time : 237.862 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 461.931 Seconds
(without alignments)
2517.530 Million cell updates/sec

Title: US-10-007-255-9

Perfect score: 24
Sequence: 1 cttatgtagacacgctttcaag 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl: *
1: gb_ba: *
2: gb_hc: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_pl: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_srs: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	AX504306	AX504306 Sequence
2	24	100.0	24	AX504323	AX504323 Sequence
3	24	100.0	568	AR080195	AR080195 Sequence
4	24	100.0	633	AX701741	AX701741 Sequence
5	24	100.0	976	HUMMDRIA02	M29423 Human P-gly
6	24	100.0	976	GI9985	GI9985 srsS10 Eric
7	24	100.0	1318	AR080194	AR080194 Sequence
8	24	100.0	1327	HUMMDRIA1	L07624 Human multi
9	24	100.0	1688	AR080193	AR080193 Sequence
10	24	100.0	2090	AR080192	AR080192 Sequence
11	24	100.0	2117	A38669	A38669 Sequence 1
12	24	100.0	2186	HUMMDRIA	M57450 Human multi
13	24	100.0	2292	CQ806551	CQ806551 Sequence
14	24	100.0	2292	AX457064	AX457064 Sequence
15	24	100.0	2292	AX598697	AX598697 Sequence
16	24	100.0	2292	AX767353	AX767353 Sequence
17	24	100.0	2292	AX795658	AX795658 Sequence
18	24	100.0	2292	AX822109	AX822109 Sequence
19	24	100.0	2292	AX825749	AX825749 Sequence

C 20	24	100.0	2292	9	HSMMDRIA
C 21	24	100.0	177380	6	AX706985
C 22	24	100.0	177380	6	AX707915
C 23	24	100.0	177380	9	AC002457
C 24	23	95.8	23	6	AX504348
C 25	23	95.8	23	6	AX504352
C 26	22	91.7	22	6	AX504349
C 27	22	91.7	22	6	AX504353
C 28	21	87.5	21	6	AX504350
C 29	21	87.5	21	6	AX504351
C 30	21	87.5	21	6	AX504354
C 31	20.8	86.7	110000	2	AC109672
C 32	20.4	85.0	158344	2	CR352257
C 33	20	83.3	20	6	AX504355
C 34	19.8	82.5	633	6	AX701744
C 35	19.8	82.5	2010	6	AX457065
C 36	19.8	82.5	2932	6	CQ806797
C 37	19.8	82.5	2932	6	AX529569
C 38	19.8	82.5	2932	6	AX598827
C 39	19.8	82.5	2932	6	AX767413
C 40	19.8	82.5	2932	6	AX795733
C 41	19.8	82.5	2932	6	AX822241
C 42	19.8	82.5	2932	6	AX825881
C 43	19.8	82.5	110000	2	AC130739
C 44	19.8	82.5	164545	2	CR354542
C 45	19.8	82.5	174986	5	AL935126

ALIGNMENTS

RESULT 1	AX504306	AX504306	Sequence 9 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504306	AX504306	AX504306				
DEFINITION	AX504306	AX504306	AX504306				
ACCESSION	AX504306	AX504306	AX504306				
VERSION	AX504306.1	GI:23386124					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
Query Match							
Best Local Similarity							
Matches							
0y	1	CTTATGTAGACACGCTTTCAAG	24				
Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
Query Match							
Best Local Similarity							
Matches							
0y	1	CTTATGTAGACACGCTTTCAAG	24				
Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
Query Match							
Best Local Similarity							
Matches							
0y	1	CTTATGTAGACACGCTTTCAAG	24				
Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
Query Match							
Best Local Similarity							
Matches							
0y	1	CTTATGTAGACACGCTTTCAAG	24				
Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
ORIGIN							
Query Match							
Best Local Similarity							
Matches							
0y	1	CTTATGTAGACACGCTTTCAAG	24				
Db	1	CTTATGTAGACACGCTTTCAAG	24				
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LOCUS	AX504323	AX504323	AX504323				
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ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
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ORGANISM							
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Best Local Similarity							
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Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
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REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
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Best Local Similarity							
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Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
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Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
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VERSION	AX504323.1	GI:23386135					
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JOURNAL							
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source							
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Query Match							
Best Local Similarity							
Matches							
0y	1	CTTATGTAGACACGCTTTCAAG	24				
Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
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REFERENCE							
AUTHORS							
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FEATURES							
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Best Local Similarity							
Matches							
0y	1	CTTATGTAGACACGCTTTCAAG	24				
Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
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ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
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JOURNAL							
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Best Local Similarity							
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0y	1	CTTATGTAGACACGCTTTCAAG	24				
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RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
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AUTHORS							
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Best Local Similarity							
Matches							
0y	1	CTTATGTAGACACGCTTTCAAG	24				
Db	1	CTTATGTAGACACGCTTTCAAG	24				
RESULT 2	AX504323	AX504323	Sequence 26 from Patent WO0234291.	24 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504323	AX504323	AX504323				
DEFINITION	AX504323	AX504323	AX504323				
ACCESSION	AX504323	AX504323	AX504323				
VERSION	AX504323.1	GI:23386135					
KEYWORDS							
SOURCE							

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
Colgan, S.P.
Compositions and methods for treating hematologic malignancies and multiple drug resistance
Patent: WO 0234291-A 26 02-MAY-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)

JOURNAL
Location/Qualifiers
1. 24
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTCAAG 24
24 CTTATGTAGACACGCTTTCAAG 1

Db 24 CTTATGTAGACACGCTTTCAAG 1

RESULT 3
AR080195/c 568 bp DNA linear PAT 31-AUG-2000

LOCUS AR080195
DEFINITION Sequence 4 from patent US 5968735.
ACCESSION AR080195
VERSION AR080195.1 GI:10006930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 568)
AUTHORS Stein, U. and Walther, W.
TITLE Vector for the expression of therapy-relevant genes
JOURNAL Patent: US 5968735-A 4 19-OCT-1999;
FEATURES
Location/Qualifiers
1..568
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 568;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTCAAG 24
203 CTTATGTAGACACGCTTTCAAG 180

Db 203 CTTATGTAGACACGCTTTCAAG 180

RESULT 4
AX701741/c 633 bp DNA linear PAT 03-APR-2003

LOCUS AX701741
DEFINITION Sequence 3 from Patent WO03002760.
ACCESSION AX701741
VERSION AX701741.1 GI:29537273
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Distler, J. and Leu, E.
TITLE Method for detecting cytosine methylation by comparatively analysing single strands of amplification
JOURNAL Patent: WO 03002760-A 3 09-JAN-2003;
FEATURES
Location/Qualifiers
1..633
/organism="synthetic construct"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 633;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTCAAG 24
211 CTTATGTAGACACGCTTTCAAG 188

Db 211 CTTATGTAGACACGCTTTCAAG 188

RESULT 5
HUMMDR1A02/c 976 bp DNA linear PRI 08-JAN-1995

LOCUS HUMMDR1A02
DEFINITION Human P-glycoprotein (MDR1) gene, 5' flank.
ACCESSION M29423 J05168 M18754
VERSION M29423.1 GI:187472
KEYWORDS P-glycoprotein; multidrug resistance.
SEGMENT 2 of 26
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 976)
AUTHORS Ueda, K., Pastan, I., and Gottesman, M.M.
TITLE Isolation and sequence of the promoter region of the human multidrug-resistance (P-glycoprotein) gene
JOURNAL J. Biol. Chem. 262 (36), 17432-17436 (1987)
MEDLINE 88087023
PUBMED 2891692
REFERENCE 2 (bases 1 to 976)
AUTHORS Chen, C.-J., Clark, D., Ueda, K., Pastan, I., Gottesman, M.M. and Roninson, I.B.
TITLE Genomic organization of the human multidrug resistance (MDR1) gene and origin of P-glycoproteins
JOURNAL J. Biol. Chem. 265 (1), 506-514 (1990)
MEDLINE 90094448
PUBMED 1967175
COMMENT Original source text: Human multidrug resistant cell line KB-V1 DNA.
[2] revises [1].
Draft entry and computer-readable sequence for [1] kindly submitted by I.B. Roninson, 27-OCT-1989.
Location/Qualifiers
1..976
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="7g21"
prim_transcript <1..>976
/gene="PGY1"
/note="PGY1 mRNA and intron (alt.); G00-120-712"
intron <1..244
/gene="PGY1"
/note="PGY1, intron A"
prim_transcript 435..>976
/gene="PGY1"
/note="PGY1 mRNA and intron (alt.)"
intron 569..>976
/gene="PGY1"
/note="PGY1, intron A"

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 976;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTCAAG 24
189 CTTATGTAGACACGCTTTCAAG 166

Db 189 CTTATGTAGACACGCTTTCAAG 166

RESULT 6
 G19985/c
 LOCUS
 DEFINITION
 G19985 976 bp DNA linear STS 28-SEP-1998
 sms10 Eric D. Green Homo sapiens STS genomic, sequence tagged site

ACCESSION
 G19985
 VERSION
 G19985.1 GI:1254684
 KEYWORDS
 STS.

SOURCE
 Homo sapiens (human)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 1 (bases 1 to 976)
 Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F., Weintrub, L.A., Mohr-Tidwell, R.M., Peluso, D.C., Fulton, R.S., Leckie, M.P. and Green, E.D.
 A collection of 1814 human chromosome 7-specific STS
 Genome Res. 7 (1), 59-64 (1997)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 9037602
 97189344

REFERENCE
 2 (bases 1 to 976)
 Green, E.D.
 Human chromosome 7 STS (1997)
 Unpublished (1997)

AUTHORS
 JOURNAL
 COMMENT
 Synonyms: PGY1
 GDB: GDB:583426
 GDB DSEG: PGY1
 Contact: Eric D. Green
 Genome Technology Branch
 National Human Genome Research Institute/NIH
 49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
 Tel: 3014020201
 Fax: 3014024735
 Email: egreen@nhgri.nih.gov
 Primer A: AACGAGAGCCGACATCTCC
 Primer B: AGGCTTCCTGTGCAAGAG
 STS size: 180

PCR Profile:
 Presoak: 0 degrees C for 0.00 minute(s)
 Denaturation: 92 degrees C for 1.00 minute(s)
 Annealing: 68 degrees C for 2.00 minute(s)
 Polymerization: 72 degrees C for 2.00 minute(s)
 PCR Cycles: 35
 Thermal Cycler: PerkinElmer TC

Protocol:
 Template: 30-100 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/uL
 Total Vol: 5 uL

Buffer:
 MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3

FEATURES
 source
 1..976
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="7"
 /clone_lib="Eric D. Green"
 1..976
 /gene="PGY1"
 253..432

primer_bind
 primer_bind
 complement (413..432)

ORIGIN
 Query Match 100.0%; Score 24; DB 11; Length 976;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 1 CTTATGTAGACACGCTCTTCAAG 24
 |||||
 Db 189 CTTATGTAGACACGCTCTTCAAG 166

RESULT 7
 AR080194/c
 LOCUS
 DEFINITION
 AR080194 Sequence 3 from patent US 5968735.
 AR080194
 ACCESSION
 AR080194.1 GI:10006929
 VERSION
 AR080194.1
 KEYWORDS
 SOURCE
 Unknown.
 ORGANISM
 Unknown.
 Unclassified.

REFERENCE
 AUTHORS
 Stein, U. and Walther, W.
 TITLE
 Vector for the expression of therapy-relevant genes
 JOURNAL
 Patent: US 5968735-A 3 19-OCT-1999;
 FEATURES
 location/Qualifiers
 1..1318
 /organism="Unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 100.0%; Score 24; DB 6; Length 1318;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 1 CTTATGTAGACACGCTCTTCAAG 24
 |||||
 Db 953 CTTATGTAGACACGCTCTTCAAG 930

RESULT 8
 HUMMDR1P/c
 LOCUS
 DEFINITION
 Human multidrug resistant P glycoprotein (MDR1, PGY1) gene, 5' flank.
 L07624
 L07624.1 GI:187500
 VERSION
 MDR1 gene; P-glycoprotein; multidrug resistance protein.
 KEYWORDS
 SOURCE
 Homo sapiens (human)

ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS
 1 (bases 1 to 1327)
 Madden, M.J., Morrow, C.S., Nakagawa, M., Goldsmith, M.E., Faichild, C.R. and Cowan, K.H.
 Identification of 5' and 3' sequences involved in the regulation of transcription of the human mdr1 gene in vivo
 J. Biol. Chem. 268 (11), 8290-8297 (1993)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 8096520

COMMENT
 Original source text: Homo sapiens (tissue library: lambda Charon 4a) bone marrow DNA.
 location/Qualifiers
 1..1327
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="7q21"
 /cell_type="Leukocyte"

gene /tissue_type="bone marrow"
/tissue_lib="lambda Charon 4a"
863..1171
/gene="PGY1"

protein_bind

/gene="PGY1"
863..875
/note="G00-120-712"
/bound_moiety="unknown"
/function="heat shock element"
930..937
/gene="PGY1"

protein_bind

/note="G00-120-712"
/bound_moiety="unknown"
/function="metal responsive element"
931..938
/gene="PGY1"

GC_signal

GC_signal

CAAT_signal

mRNA

exon

mRNA

protein_bind

intron

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 1327;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 791 CTTATGTAGACACGCTTTCAAG 768

RESULT 9
AR080193/c 1688 bp DNA 1linear PAT 31-AUG-2000

LOCUS AR080193
DEFINITION Sequence 2 from patent US 5968735.

ACCESSION AR080193
VERSION AR080193.1 GI:10006928

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 1688)

AUTHORS Stein,U. and Walther,W.

TITLE Vector for the expression of therapy-relevant genes

JOURNAL Patent: US 5968735-A 2 19-OCT-1999;

FEATURES

1..1688
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 1688;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 1323 CTTATGTAGACACGCTTTCAAG 1300

RESULT 10
AR080192/c 2090 bp DNA 1linear PAT 31-AUG-2000

LOCUS AR080192
DEFINITION Sequence 1 from patent US 5968735.

ACCESSION AR080192
VERSION AR080192.1 GI:10006927

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 2090)

AUTHORS Stein,U. and Walther,W.

TITLE Vector for the expression of therapy-relevant genes

JOURNAL Patent: US 5968735-A 1 19-OCT-1999;

FEATURES

1..2090
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 2090;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTCAAG 24
Db 1725 CTTATGTAGACACGCTTTCAAG 1702

RESULT 11
A38669/c 2117 bp DNA 1linear PAT 11-NOV-1999

LOCUS A38669
DEFINITION Sequence 1 from Patent WO9411522.

ACCESSION A38669
VERSION A38669.1 GI:2295152

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS Stein,U. and Walther,W.

TITLE VECTOR FOR THE EXPRESSION OF THERAPY-RELEVANT GENES

JOURNAL Patent: WO 9411522-A 1 26-MAY-1994;

MAX DELBRUECK CT FUER MOLEKULA (DE)

Other publication DE 4238778 940519.

COMMENT

location/Qualifiers

1..2117

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/clone="CVS-SW1"

/cell_type="SARCOMAS"

/tissue_type="TUMORS"

variation

2076

/replace="c"

2110

/replace="c"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 2117;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24
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 DB 1725 CTTATGTAGACACGCTTTTCAAG 1702

RESULT 12
 HUMMDRIA/c 2186 bp DNA linear PRI 07-JAN-1995
 LOCUS Human multidrug-resistance (MDR1) gene, exon 1.
 DEFINITION M57450 J05673
 ACCESSION M57450.1 GI:187470
 VERSION multidrug resistance.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Kohno, K., Sato, S., Uchiumi, T., Takano, H., Kato, S. and Kuwano, M.
 TITLE Tissue-specific enhancer of the human multidrug-resistance (MDR1) gene

JOURNAL J. Biol. Chem. 265 (32), 19690-19696 (1990)

MEDLINE 91060578

PUBMED 1978833

COMMENT Original source text: Human cancer multidrug-resistant cell line KB-C1 DNA.

FEATURES
 source location/Qualifiers

1..2186
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="7q21"
 /cell_line="KB-C1"
 /tissue_type="KB cancer"
 623..627
 /standard_name="5' insertion target sequence"
 628..950
 title="Alu repeat"
 /rpt_family="Alu repeat"
 951..955
 /standard_name="3' insertion target sequence"
 2029..2186
 /gene="PGY1"
 2029..2158
 /gene="PGY1"
 /product="multidrug resistance protein"
 /note="G00-120-712"
 2159..2186
 /gene="PGY1"
 /note="G00-120-712"
 /number=1

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 2186;
 Best Local Similarity 100.0%; Pred. No. 0.95;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24
 |||||
 DB 1780 CTTATGTAGACACGCTTTTCAAG 1757

RESULT 13
 CQ806551 2932 bp DNA linear PAT 10-MAY-2004
 LOCUS CQ806551/c
 DEFINITION Sequence 1 from Patent WO2004035803.
 ACCESSION CQ806551
 VERSION CQ806551.1 GI:47111933

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 Fockens, J., Harbeck, N., Koenig, T., Maier, S., Martens, J., Model, F.,

Nimmrich, I., Rujan, T., Schmitt, A., Schmitt, M., Look, M.P. and Marx, A.
 TITLE Method and nucleic acids for the improved treatment of breast cell
 JOURNAL proliferative disorders
 Patent: WO 2004035803-A 1 29-APR-2004;
 Epigenomics AG (DE)

FEATURES
 source location/Qualifiers
 1..2932
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 2932;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24
 |||||
 DB 828 CTTATGTAGACACGCTTTTCAAG 805

RESULT 14
 AX457064/c 2932 bp DNA linear PAT 06-JUL-2002
 LOCUS AX457064
 DEFINITION Sequence 25 from Patent WO231186.
 ACCESSION AX457064
 VERSION AX457064.1 GI:21715846
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Berlin, K.
 TITLE Method for the detection of cytosine methylations
 JOURNAL Patent: WO 0231186-A 25 18-APR-2002;
 Epigenomics AG (DE)

FEATURES
 source location/Qualifiers
 1..2932
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 2932;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTTCAAG 24
 |||||
 DB 828 CTTATGTAGACACGCTTTTCAAG 805

RESULT 15
 AX598697/c 2932 bp DNA linear PAT 14-FEB-2003
 LOCUS AX598697
 DEFINITION Sequence 37 from Patent WO02077272.
 ACCESSION AX598697
 VERSION AX598697.1 GI:28398833

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J.,
 Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Ley, E.,
 Lewin, A., Lipsecher, E., Maier, S., Model, F., Mueller, V., Otto, T.,
 Pelet, C. and Ziebarth, H.

TITLE Methods and nucleic acids for the analysis of hematopoietic cell
 JOURNAL proliferative disorders
 Patent: WO 02077272-A 37 03-OCT-2002;

Epigenomics AG (DE)
 FEATURES
 Location/Qualifiers
 source 1..2932
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 100.0%; Score 24; DB 6; Length 2932;
 Best Local Similarity 100.0%; Pred. No. 0.9;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACGCTTTCAAG 24
 |||||
 Db 828 CTTATGTAGACGCTTTCAAG 805

Search completed: February 9, 2005, 17:01:53
 Job time : 464.931 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2350.9 Seconds
(without alignments)
388.593 Million cell updates/sec

Title: US-10-007-255-9
Perfect score: 24
Sequence: 1 ctatctgtagacacgtcttcaag 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapexc 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:*

1: gb_est1:*\n2: gb_est2:*\n3: gb_hc:*\n4: gb_est3:*\n5: gb_est4:*\n6: gb_est5:*\n7: gb_est6:*\n8: gb_gse1:*\n9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.4	85.0	213	7	CN813365 Fg06_06h1
2	19.8	82.5	671	2	BB662530 BB662530
3	19.2	80.0	780	8	BZ984511 PUGIE79TD
4	19.2	80.0	780	8	CC365078 PUMME62TB
5	19.2	80.0	819	9	BZ984507 PUGIE79TB
6	19.2	80.0	889	9	CG457221 PUKIG34TD
7	18.8	78.3	426	6	CD476851 eca01-18m
8	18.8	78.3	627	9	BH332334 CH230-125
9	18.8	78.3	632	9	CL706910 OR_BBA002
10	18.8	78.3	632	9	CL706910 OR_BBA002
11	18.8	78.3	731	9	CL706910 OR_BBA002
12	18.8	78.3	765	9	CL807004 OR_Cha002
13	18.4	76.7	526	1	AI332619 qg28a04.x
14	18.2	75.8	180	8	BH812962 SALX_0635
15	18.2	75.8	197	8	BZ290962 SALX_1122
16	18.2	75.8	241	2	AM999627 MR0-BN007
17	18.2	75.8	323	1	TS3393 yb47c09.r1
18	18.2	75.8	353	1	AV790780 AV790780
19	18.2	75.8	433	7	N96634 21309 lambda
20	18.2	75.8	433	8	CC053247 SALX_0412
21	18.2	75.8	513	4	BI813622 L002D03.O
22	18.2	75.8	539	7	CV070774 CS_g11_30
23	18.2	75.8	575	1	AV558834 AV558834
24	18.2	75.8	596	7	CV071055 CS_g11_39

C 25	18.2	75.8	652	8	BZ845681	BZ845681 CH240_291
C 26	18.2	75.8	672	1	A1729367	A1729367 BNLG1131
C 27	18.2	75.8	685	9	AG044289	AG044289 Pan troy1
C 28	18.2	75.8	686	4	BG440031	BG440031 GA_EA000
C 29	18.2	75.8	691	2	BB045461	BB045461 BB045461
C 30	18.2	75.8	720	6	CB669495	CB669495 OSUN602A
C 31	18.2	75.8	737	6	CB669534	CB669534 OSUN602B
C 32	18.2	75.8	749	4	BI737199	BI737199 603358225
C 33	18.2	75.8	759	3	CNS0A6C1	BX825649 Arabidops
C 34	18.2	75.8	811	9	CNS06DK0	AL393936 T7 end of
C 35	18.2	75.8	975	9	CR012766	CR012766 Forward B
C 36	18.2	75.8	986	9	CR248215	CR248215 Forward B
C 37	18.2	75.8	1474	6	CA156945	CA156945 SCEOR2302
C 38	18.2	75.8	512	8	AQ020267	AQ020267 CIT-HSP-2
C 39	18.2	75.8	569	8	BZ603334	BZ603334 WHAC067TF
C 40	17.8	74.2	516	7	CK507205	CK507205 rswcc0.01
C 41	17.8	74.2	542	2	BF195858	BF195858 7086B09.x
C 42	17.8	74.2	542	2	BF197586	BF197586 7085B09.x
C 43	17.8	74.2	555	8	AZ009974	AZ009974 RPCI-23-2
C 44	17.8	74.2	559	9	CR343395	CR343395 Medicago
C 45	17.8	74.2	585	9	CL376034	CL376034 RPCI44_44

ALIGNMENTS

RESULT 1
CN813365/c 213 bp mRNA linear EST 01-JUN-2004
LOCUS Fg06_06h10_R Fg06_AAPC_ECORC Fusarium graminearum perithecia
DEFINITION Gibberella zeae cDNA clone Fg06_06h10, mRNA sequence.

ACCESSION CN813365
VERSION CN813365.1 GI:47837376

KEYWORDS SOURCE ORGANISM

Gibberella zeae (anamorph: Fusarium graminearum)
Gibberella zeae

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE 1 (bases 1 to 213)
Harris,L.J., Rochelleau,H., Ouellet,T., Allard,S., Chapados,J.,

Couroux,P., De Moore,A., Hattori,J.I., Lacroix,C., Masotti,M., Robert,L.S., Singh,J.A., Spriett,D. and Tinker,N.A.

Expressed Sequence Tags from Fusarium graminearum enriched for late stage perithecia

Unpublished (2004)

JOURNAL CONTACT: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada
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CANADA
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Fax: (613) 759-6566
Email: harris@agr.gc.ca.

FEATURES
source location/Qualifiers

1..213
/organism="Gibberella zeae"

/mol_type="mRNA"
/strain="DAOM 180378"

/db_xref="taxon:5518"
/clone="Fg06_06h10"

/dev_stage="Sexual"
/lab_host="E. coli DH10B"

/clone_lib="Fg06_AAPC_ECORC_Fusarium graminearum perithecia"

/note="Vector: pGem-T easy; Site 1: EcoRI; Mycelia grown on carrot agar at 200C until confluent; perithecia induced with Tween 40 solution (25% v/v). Fruiting bodies were collected 20 days after induction. Total RNA was extracted using Trizol. cDNAs were amplified using Invitrogen Generacer kit. cDNA was not fractionated and was bidirectionally cloned."

ORIGIN

Query Match 85.0%; Score 20.4; DB 7; Length 213;
 Best Local Similarity 95.5%; Pred. No. 50;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 TATGTAGACAGCTCTTTCAAG 24
 |||||
 186 TATGTAGACAGCTTTCAAG 165

RESULT 2
 BB662530/c 671 bp mRNA linear EST 26-OCT-2001
 DEFINITION BB662530 RIKEN full-length enriched, 15 days embryo head Mus
 musculus cDNA clone D93005N11 5', mRNA sequence.
 BB662530
 BB662530.1 GI:16496284
 EST
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 671)
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
 Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
 and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multiplexed sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I.,
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.
 Location/Qualifiers
 1..671
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="D93005N11"
 /sex="mixed"
 /tissue_type="head"

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source

Location/Qualifiers
 1..671
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="D93005N11"
 /sex="mixed"
 /tissue_type="head"

/dev_stage="15 days embryo"
 /lab_host="PH105"
 /clone_lib="RIKEN full-length enriched, 15 days embryo
 head"
 /note="Site 1: Salt; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5',
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGAGAGAGATTCGAGTTAATTAATTAATTCCTCCCTCCCTCC 3']. cDNA
 was cloned into the XhoI and BamHI sites. Vector: a
 modified pBluescript KS(+) after bulk excision from Lambda
 phage I"

Query Match 82.5%; Score 19.8; DB 2; Length 671;
 Best Local Similarity 91.3%; Pred. No. 1,1e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 TTATGTAGACAGCTCTTTCAAG 24
 |||||
 472 TTATGTAGACAGCTTTCAAG 450

RESULT 3
 BZ984511 780 bp DNA linear GSS 25-MAR-2003
 DEFINITION PUGIE797D ZM.0.6.1.0 KB Zea mays genomic clone ZMMBTa390M13,
 genomic survey sequence.
 BZ984511
 BZ984511.1 GI:29219382
 GSS.
 VERSION BZ984511.1 GI:29219382
 KEYWORDS Zea mays
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 780)
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
 Resnick, A., Frazer, C.M., Juan, Y., San Miguel, P., Ma, J. and
 Bennettzen, J.
 Maize Genomics Consortium
 Unpublished (2003)
 Other GSSs: PUGIE797B
 Contact: Cathy Whitelaw
 TIGR

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@cigr.org
 Seq primer: TP
 Class: shared ends.

FEATURES

source

Location/Qualifiers
 1..780
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBTa390M13"
 /clone_lib="ZM.0.6.1.0 KB"
 /note="Vector: pCR4-TOP0; Site 1: EcoRI; 0.6-1.0 kb high
 Cor selected genomic DNA library"

ORIGIN

Query Match 80.0%; Score 19.2; DB 8; Length 780;
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CTTATGTAGACACGCTTTTCAAG 24
 |||||
 380 CTTATGTAGACATGCTTTTCAAG 403

RESULT 4
 CC365078 780 bp DNA linear GSS 16-MAY-2003
 LOCUS PUHME62TB.ZM.0.6.1.0_KB_Zea_mays_genomic_clone_ZMMBTA483K03,
 DEFINITION genomic survey sequence.
 ACCESSION CC365078
 VERSION CC365078.1 GI:30834478
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 780)
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennetzen,J.
 Maize Genomics Consortium
 Unpublished (2003)
 Other GSSs: PUHME62TD
 Contact: Cathy WhiteJaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteJaw@tigr.org
 Seq primer: TR
 Class: sheared ends.

FEATURES
 source
 1..780
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_id="ZMMBTA483K03"
 /clone_lib="ZM.0.6.1.0_KB"
 /note="Vector: PCR4-TOPO, Site_1: EcoRI, 0.6-1.0 kb high
 Cor selected genomic DNA library"

ORIGIN
 Query Match 80.0%; Score 19.2; DB 8; Length 780;
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTTATGTAGACACGCTTTTCAAG 24
 |||||
 103 CTTATGTAGACATGCTTTTCAAG 80

RESULT 5
 BZ984507 816 bp DNA linear GSS 25-MAR-2003
 LOCUS PUGIE79TB.ZM.0.6.1.0_KB_Zea_mays_genomic_clone_ZMMBTA390M13,
 DEFINITION genomic survey sequence.
 ACCESSION BZ984507
 VERSION BZ984507.1 GI:29219374
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 816)
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennetzen,J.

TITLE Maize Genomics Consortium
 JOURNAL Unpublished (2003)
 COMMENT Other_GSSs: PUGIE79TD
 Contact: Cathy WhiteJaw
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 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteJaw@tigr.org
 Seq primer: TR
 Class: sheared ends.

FEATURES
 source
 1..816
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_id="ZMMBTA390M13"
 /clone_lib="ZM.0.6.1.0_KB"
 /note="Vector: PCR4-TOPO, Site_1: EcoRI, 0.6-1.0 kb high
 Cor selected genomic DNA library"

ORIGIN
 Query Match 80.0%; Score 19.2; DB 8; Length 816;
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CTTATGTAGACACGCTTTTCAAG 24
 |||||
 620 CTTATGTAGACATGCTTTTCAAG 597

RESULT 6
 CG457221 889 bp DNA linear GSS 17-SEP-2003
 LOCUS PUIK34TDB.ZM.0.6.1.0_KB_Zea_mays_genomic_clone_ZMMBTA0602F19,
 DEFINITION genomic survey sequence.
 ACCESSION CG457221
 VERSION CG457221.1 GI:34842221
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 889)
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennetzen,J.
 Maize Genomics Consortium
 Unpublished (2003)
 Other_GSSs: PUIK34TDB
 Contact: Cathy WhiteJaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteJaw@tigr.org
 Seq primer: TR
 Class: sheared ends.

FEATURES
 source
 1..889
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_id="ZMMBTA0602F19"
 /clone_lib="ZM.0.6.1.0_KB"
 /note="Vector: PCR4-TOPO, Site_1: EcoRI, 0.6-1.0 kb high
 Cor selected genomic DNA library"

ORIGIN
 Query Match 80.0%; Score 19.2; DB 9; Length 889;

Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTTATGTAGACACGCTTTCAAG 24
|||||
550 CTTATGTAGACACGCTTTCAAG 573

RESULT 7

CL745575

LOCUS CL745575 426 bp DNA linear GSS 27-JUL-2004
DEFINITION OR_BB40082M07.r OR_BBA Oryza rufipogon genomic clone OR_BB40082M07

ACCESSION CL745575
VERSION CL745575.1 GI:50686923

KEYWORDS GSS
SOURCE

ORGANISM

Oryza rufipogon

Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 426)

AUTHORS Kim,H., Yu,Y., Stum,D., Yeat,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

TITLE OMA Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161 Std Error: 0.00
Plate: 0082 row: M column: 07
Seq primer: CAC TCA TTA GGC ACC CCA

Class: BAC ends.
Location/Qualifiers

FEATURES

source

1..426
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BB40082M07"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 78.3%; Score 18.8; DB 9; Length 426;
Best Local Similarity 90.9%; Pred. No. 3.3e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TATGTAGACACGCTTTCAAG 24
|||||
151 TATGTAGACACGCTTTCAAG 172

RESULT 8

CD476851

LOCUS CD476851 464 bp mRNA linear EST 04-JUN-2003
DEFINITION eca01-18ms1-f06 Eca01 Eschscholzia californica cDNA clone

ACCESSION CD476851
VERSION CD476851
KEYWORDS eca01-18ms1-f06 5', mRNA sequence.

SOURCE CD476851.1 GI:31398119
EST.

Eschscholzia californica (California poppy)

Eschscholzia californica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;

REFERENCE

AUTHORS

Papaveraceae; Eschscholziaceae; Eschscholzia.
1 (bases 1 to 464)
deBamphilis,C., Carlson,J., Ma,H., Tanksley,S., Field,D.,
Leebens-Mack,J., Arrington,J., Zahn,L.M., Kong,H., Iluv,D.,
Druckemiller,M., Landherr,L., Hu,Y., Plock,S., Wall,K.,
Chioean,S., Albert,Y., Doyle,J., Frolich,M., Miller,M.,
Oppenheimer,D., Solis,D., Solis,P. and Theissen,G.
Generation of ESTs from early flower buds of Eschscholzia
californica

TITLE

JOURNAL

COMMENT

Unpublished (2002)
Contact: Claude deBamphilis or James Leebens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhl10@psu.edu

The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: eca01-18ms1 row: f column: 06
Seq primer: M13F.

FEATURES

source

1..464
/organism="Eschscholzia californica"
/mol_type="mRNA"
/cultivar="Aurantia Orange"
/db_xref="taxon:3467"
/clone="eca01-18ms1-f06"
/issue_type="flower buds <= 2.5mm"
/dev_stage="millimeter buds"
/lab_host="SOLR"
/clone_lib="eca01"
/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
Site 2: XhoI; plants were grown in greenhouses at Penn
State from commercially available seeds. Only floral buds
with diameter of 2.5 mm or less were collected. This is a
directionally cloned, non-normalized library. Avg. insert
length: 1702; Primers: M13F and M13R; Antibiotic: 50 ug/ml
Ampicillin; Primary Titer: 766 pfu total; Amplified Titer:
1.68E11 pfu/ml; Mass Excised Titer: 5.6E8 total; This
library has been generated by the Floral Genome Project
(FGP). We would like to thank Huck Life Sciences
Consortium for their assistance. The Floral Genome Project
is funded by NSF's Plant Genome Research Program
(DBI-0115684). More information about the project can be
obtained at http://fgp.bio.psu.edu"

ORIGIN

Query Match 78.3%; Score 18.8; DB 6; Length 464;
Best Local Similarity 90.9%; Pred. No. 3.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TATGTAGACACGCTTTCAAG 24
|||||
332 TATGTAGACACGCTTTCAAG 311

RESULT 9

BH332334

LOCUS BH332334 627 bp DNA linear GSS 03-DEC-2001
DEFINITION CH230-125M16_TV CHORI-230 Segment 1 Rattus norvegicus genomic clone

ACCESSION BH332334
VERSION BH332334
KEYWORDS BH332334.1 GI:17263048

SOURCE BH332334.1 GI:17263048
Rattus norvegicus (Norway rat)

Eschscholzia californica

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 627)

AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregorjls, E., Ovetton, L., Russell, D., Chen, D., R. 1998, F., de Jong, P., and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcorI segment
Unpublished (1999)
Other GSSs: CH230-125M16.TV
Contact: Shuying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igir.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pierec de Jong (pjejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering/information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 125 Row: M Column: 16
Seq primer: 17
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..627
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SENHsd/MCM"
/db_xref="taxon:10116"
/clone="CH230-125M16"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcorI; Site_2: EcorI;
CHORI-230 Rat (BN/SENHsd/MCM) BAC library produced by
Pierec de Jong"

ORIGIN
Query Match 78.3%; Score 18.8; DB 8; Length 627;
Best Local Similarity 90.9%; Pred. No. 3.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTATGTAGACAGCTCTTCAAA 23
|||||
322 TTATGTAGACAGCTCTTCAAGA 343

Db

RESULT 10
CL706910 632 bp DNA linear GSS 26-JUL-2004
LOCUS OR_BBA0024M03.r OR_BBA Oryza rufipogon genomic clone OR_BBA0024M03
DEFINITION 3', genomic survey sequence.
ACCESSION CL706910
VERSION CL706910.1 GI:50593948
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 632)
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA TGA GG
REVERSE: TAA TAC GAC TCA TGA GG

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0024 row: M column: 03
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..632
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBA0024M03"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 78.3%; Score 18.8; DB 9; Length 632;
Best Local Similarity 90.9%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TATGTAGACAGCTCTTCAAG 24
|||||
151 TATGTAGACAGCTCTTCAAG 172

Db

RESULT 11
CL720267 731 bp DNA linear GSS 26-JUL-2004
LOCUS OR_BBA0048E12.f OR_BBA Oryza rufipogon genomic clone OR_BBA0048E12
DEFINITION 5', genomic survey sequence.
ACCESSION CL720267
VERSION CL720267.1 GI:50611301
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 731)
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA TGA GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0048 row: E column: 12
Seq primer: TAA TAC GAC TCA TGA GG
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..731
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_BBA0048E12"
/issue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 78.3%; Score 18.8; DB 9; Length 731;
Best Local Similarity 90.9%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TATGTAGACACGCTTTTCAAG 24
 |||||
 DB 151 TATGTGACTCGCTTTTCAAG 172

RESULT 12
 CL807004/c 765 bp DNA linear GSS 09-AUG-2004
 LOCUS OR_CBA0020P06.f OR_CBA Oryza rufipogon genomic clone OR_CBA0020P06
 DEFINITION 5', genomic survey sequence.
 ACCESSION CL807004.1 GI:51044586
 VERSION CL807004.1
 KEYWORDS GSS.
 SOURCE Oryza rufipogon
 ORGANISM Oryza rufipogon
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 1 (bases 1 to 765)
 Kim, H., Yu, Y., Waisetski, M., Yost, D., Spum, D., Rao, K., Luo, M.,
 Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and
 Wang, R.
 OMAE project
 Unpublished (2004)
 Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: http://genome.arizona.edu
 PCR primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Plate: 0020 row: P column: 06
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.
 Location/Qualifiers
 1..765
 /organism="Oryza rufipogon"
 /mol_type="genomic DNA"
 /db_xref="taxon:4529"
 /clone="OR_CBA0020P06"
 /rissue_type="young leaves"
 /dev_stage="2 week old seedlings"
 /lab_host="DH10B T1 phage resistant"
 /clone_lib="OR_CBA"
 /note="Vector: pAGIRAC1; Site_1: HindIII; Site_2: HindIII;
 dir created 36 hrs before harvest"

ORIGIN

Query Match 78.3%; Score 18.8; DB 9; Length 765;
 Best Local Similarity 90.9%; Pred. No. 3.5e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TATGTAGACACGCTTTTCAAG 24
 |||||
 DB 152 TATGTGACTCGCTTTTCAAG 131

RESULT 13
 A1332619 526 bp mRNA linear EST 13-FEB-1999
 LOCUS gq28a04.x1 Soares NHMPU S1 Homo sapiens cDNA clone IMAGE:1933806
 DEFINITION 3' similar to SW:MP1_RABIT P31429 MICROSOMAL DIPEPTIDASE PRECURSOR
 // mRNA sequence.
 ACCESSION A1332619
 VERSION A1332619.1 GI:4069178
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 526)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-rc@mail.nih.gov.
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1131 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 412.
 Location/Qualifiers
 1..526
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1933806"
 /rissue_type="pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares NHMPU S1"
 /note="Organ: mixed (see below); Vector: pT7T3D-Pac
 (pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Eco RI. Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NDH, pregnant uterus
 NDHPV, and fetal heart NDH19W) were mixed, and 88 circles
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

ORIGIN

Query Match 76.7%; Score 18.4; DB 1; Length 526;
 Best Local Similarity 95.0%; Pred. No. 5.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TATGTAGACACGCTTTTCA 22
 |||||
 DB 474 TATGTGACACGCTTTTCA 493

RESULT 14
 BH812962 180 bp DNA linear GSS 02-MAY-2002
 LOCUS SALK_063510 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 DEFINITION thaliana genomic clone SALK_063510, genomic survey sequence.
 ACCESSION BH812962
 VERSION BH812962.1 GI:20391417
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 180)
 Alonso, J.M., Leisbe, T.J., Barajas, P., Chen, H., Cheuk, R.,
 Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
 Shinn, P., Zimmerman, J., and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckers@salk.edu
 This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 3' end of
 At3g26850.
 Class: TDNA tagged.
 Location/Qualifiers
 1. 180
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_063510"
 /clone_1b="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 75.8%; Score 18.2; DB 8; Length 180;
 Best Local Similarity 87.0%; Pred. No. 5.8e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACACGCTTTCAAG 24
 |||||
 Db 100 TTATGTAGACAGTATGTCAAG 78

RESULT 15

BZ290962 197 bp DNA linear GSS 24-OCT-2002
 LOCUS SALK_112237.50.25.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_112237.50.25.x, genomic
 survey sequence.

ACCESSION BZ290962
 VERSION BZ290962.1 GI:24335370
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 197)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the

TITLE Arabidopsis Genome
 Arabidopsis Genome
 Unpublished (2001)

JOURNAL Contact: Joseph R. Ecker
 COMMENT Salk Institute Genomic Analysis Laboratory (SIGNAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 3' end of
 At3g26850.
 Class: TDNA tagged.

FEATURES
 source Location/Qualifiers
 1. 197

/organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_112237.50.25.x"
 /clone_1b="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 75.8%; Score 18.2; DB 8; Length 197;
 Best Local Similarity 87.0%; Pred. No. 5.9e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTATGTAGACACGCTTTCAAG 24
 |||||
 Db 98 TTATGTAGACAGTATGTCAAG 76

Search completed: February 9, 2005, 21:55:30
 Job time : 2354.9 secs

... Page Blank (uspto)

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Colgan, S.P.

JOURNAL Title Compositions and methods for treating hematologic malignancies and multiple drug resistance

Patent: WO 0234291-A 27 02-MAY-2002;

THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)

FEATURES Location/Qualifiers

1..25

1. .351

Source /organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCCAAGCCCGGCGCTG 25

Db 25 GTGCTCAGCCCAAGCCCGGCGCTG 1

RESULT 3

LOCUS AR080196/c 351 bp DNA linear PAT 31-AUG-2000

DEFINITION Sequence 5 from patent US 5968735.

ACCESSION AR080196

VERSION AR080196.1 GI:10006931

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 351)

AUTHORS Stein, U. and Walthers, W.

TITLE Vector for the expression of therapy-relevant genes

JOURNAL Patent: US 5968735-A 5 19-OCT-1999;

FEATURES Location/Qualifiers

1..351

Source /organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 351;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCCAAGCCCGGCGCTG 25

Db 170 GTGCTCAGCCCAAGCCCGGCGCTG 146

RESULT 4

LOCUS AR080197/c 351 bp DNA linear PAT 31-AUG-2000

DEFINITION Sequence 6 from patent US 5968735.

ACCESSION AR080197

VERSION AR080197.1 GI:10006932

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 351)

AUTHORS Stein, U. and Walthers, W.

TITLE Vector for the expression of therapy-relevant genes

JOURNAL Patent: US 5968735-A 6 19-OCT-1999;

FEATURES Location/Qualifiers

1..351

Source /organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 351;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCCAAGCCCGGCGCTG 25

Db 170 GTGCTCAGCCCAAGCCCGGCGCTG 146

RESULT 5

LOCUS AF345623/c 370 bp mRNA linear PRI 02-MAY-2003

DEFINITION Homo sapiens MES-SA/2B-E3 MDR1 mRNA, 5'UTR.

ACCESSION AF345623

VERSION AF345623.1 GI:13591739

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 370)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

JOURNAL Miscellaneous notes on Pleurotus

PERSONA 18, 55-69 (2002)

REFERENCE 2 (bases 1 to 370)

AUTHORS Chen, G.K., Wang, Y. and Sikic, B.I.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-2001) Oncology/Medicine, Stanford University School of Medicine, 269 Campus Drive, Stanford, CA 94305-5151, USA

FEATURES Location/Qualifiers

1..370

Source /organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="7"

/map="7q21.1"

/cell_line="MES-SA/2B-E3"

/tissue_type="uterine sarcoma"

/note="doxorubicin selected cell line"

<1..>370

/gene="MDR1"

<1..>370

/gene="MDR1"

ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 370;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCCAAGCCCGGCGCTG 25

Db 250 GTGCTCAGCCCAAGCCCGGCGCTG 226

RESULT 6

LOCUS AF345624/c 370 bp mRNA linear PRI 02-MAY-2003

DEFINITION Homo sapiens MES-SA/VL20-4.2 MDR1 mRNA, 5'UTR.

ACCESSION AF345624

VERSION AF345624.1 GI:13591740

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 370)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

JOURNAL Miscellaneous notes on Pleurotus

PERSONA 18, 55-69 (2002)

REFERENCE 2 (bases 1 to 370)

AUTHORS Wang, Y., Chen, G.K. and Sikic, B.I.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-2001) Oncology/Medicine, Stanford University

Query Match 100.0%; Score 25; DB 9; Length 370;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCCAAGCCCGGCGCTG 25

Db 250 GTGCTCAGCCCAAGCCCGGCGCTG 226

School of Medicine, 269 Campus Drive, Stanford, CA 94305-5151, USA

FEATURES
Location/Qualifiers
1..370
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="7"
/map="7q21.1"
/cell_line="MES-SA/VL20-4.2"
/tissue_type="uterine sarcoma"
/note="Vlnblastine selected cell line"

gene
5'UTR
/gene="MDR1"
<1..>370
/gene="MDR1"
/gene="MDR1"

ORIGIN
Query Match 100.0%; Score 25; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTAGCCAGCCCGCGCGCTG 25
|||||
Db 250 GTGCTAGCCAGCCCGCGCGCTG 226

RESULT 7
LOCUS AR080195/c 568 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 4 from patent US 5968735.
ACCESSION AR080195
VERSION AR080195.1 GI:10006930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 568)
Stein,U. and Walther,W.
Vector for the expression of therapy-relevant genes
JOURNAL Patent: US 5968735-A 4 19-OCT-1999;
FEATURES
Location/Qualifiers
1..568
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 568;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTAGCCAGCCCGCGCGCTG 25
|||||
Db 414 GTGCTAGCCAGCCCGCGCGCTG 390

RESULT 8
LOCUS AX701741/c 633 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 3 from Patent WO03002760.
ACCESSION AX701741
VERSION AX701741.1 GI:29537273
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
1 Dietler,J. and Leu,E.
Method for detecting cytosine methylation by comparatively
analysing single strands of amplification
Patent: WO 03002760-A 3 09-JAN-2003;
JOURNML Epigenomics AG (DE)
FEATURES
Location/Qualifiers
1..633
source

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="MDR1-PCR-Produkt"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 633;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTAGCCAGCCCGCGCGCTG 25
|||||
Db 422 GTGCTAGCCAGCCCGCGCGCTG 398

RESULT 9
LOCUS HUMMDR1A02/c 976 bp DNA linear PRI 08-JAN-1995
DEFINITION Human P-glycoprotein (MDR1) gene, 5' flank.
ACCESSION M29423 J05168 M18754
VERSION M29423.1 GI:187472
KEYWORDS P-glycoprotein; multidrug resistance.
SEGMENT 2 of 26
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 976)
Ueda,K., Pastan,I. and Gottesman,M.M.
Isolation and sequence of the promoter region of the human
multidrug-resistance (P-glycoprotein) gene
J Biol. Chem. 262 (36), 17432-17436 (1987)
86087023
MEDLINE
PUBMED 2891692
2 (bases 1 to 976)
Chen,C.J., Clark,D., Ueda,K., Pastan,I., Gottesman,M.M. and
Ronsinson,I.B.

TITLE
Genomic organization of the human multidrug resistance (MDR1) gene
and origin of P-glycoproteins
J. Biol. Chem. 265 (1), 506-514 (1990)
90094448
MEDLINE
PUBMED 1967175
COMMENT
Original source text: Human multidrug resistant cell line KB-V1

DNA.
[2] revises [1].
Draft entry and computer-readable sequence for [1] kindly submitted
by I.B.Roninson, 27-OCT-1989.
Location/Qualifiers
1..976
/organism="Homo sapiens"
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Query Match 100.0%; Score 25; DB 9; Length 976;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTAGCCAGCCCGCGCGCTG 25
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Db 400 GTGCTCAGCCCAAGCCCGCGGCTG 376

RESULT 10
LOCUS G19985/c 976 bp DNA linear STS 28-SEP-1998
DEFINITION SMS10 Eric D. Green Homo sapiens STS genomic, sequence tagged site.

ACCESSION G19985
VERSION G19985.1 GI:1254684
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 976)
Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F., Weintraub, L.A., Mohr-Ridwell, R.M., Feluso, D.C., Fulton, R.S., Leckie, M.P. and Green, E.D.
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
97189344
9037602
2 (bases 1 to 976)
Green, E.D.
Human chromosome 7 STSs (1997)
Unpublished (1997)
SYNonyms: PGY1
GDB: GDB:583426
GDB DSEG: PGY1
Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Primer A: AACGAGCCAGACATCTCC
Primer B: AGGCTTCTGTGCAAGAG
STS size: 180
PCR Profile:

Presoak: 0 degrees C for 0.00 minute(s)
Denaturation: 92 degrees C for 1.00 minute(s)
Annealing: 68 degrees C for 2.00 minute(s)
Polymerization: 72 degrees C for 2.00 minute(s)
PCR Cycles: 35
Thermal Cycler: PerkinElmer TC

Protocol:

Template: 30-100 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uM
Total Vol: 5 uL

Buffer:

MgCl₂: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3

FEATURES
source
1..976
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/clone_lib="Eric D. Green"
1..976
gene

This STS was developed from sequence determined by another investigator. See GenBank record: M29423 For additional information about the NHGRI chromosome 7 mapping project, see <http://www.nhgri.nih.gov/DIR/GRB/CHR7>. Also see Genomics 11:548-64 (1991) [MUID=92128937].
Location/Qualifiers

STs /gene="PGY1"
253..432
/gene="PGY1"
253..272
primer_bind
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complement(413..432)
ORIGIN
primer_bind

Query Match 100.0%; Score 25; DB 11; Length 976;
Best Local Similarity 100.0%; Pred. NO. 17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCCAAGCCCGCGGCTG 25
|||||
Db 400 GTGCTCAGCCCAAGCCCGCGGCTG 376
|||||

RESULT 11
LOCUS AR080194/c 1318 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 3 from patent US 5968735.
ACCESSION AR080194
VERSION AR080194.1 GI:10006929
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
Stein, U. and Walther, W.
Vector for the expression of therapy-relevant genes
Patent: US 5968735-A 3 19-OCT-1999;
JOURNAL
Location/Qualifiers
1..1318
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. NO. 16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTCAGCCCAAGCCCGCGGCTG 25
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Db 1164 GTGCTCAGCCCAAGCCCGCGGCTG 1140
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RESULT 12
LOCUS HUMMDR1P/c 1327 bp DNA linear PRI 09-JAN-1995
DEFINITION Human multidrug resistant P glycoprotein (MDR1; PGY1) gene, 5' flank.
ACCESSION L07624
VERSION L07624.1 GI:187500
KEYWORDS MDR1 gene; P-glycoprotein; multidrug resistance protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1327)
Madden, M.J., Morrow, C.S., Nakagawa, M., Goldsmith, M.E., Falchid, C.R. and Cowan, K.H.
Identification of 5' and 3' sequences involved in the regulation of transcription of the human mdr1 gene in vivo
J. Biol. Chem. 268 (11), 8290-8297 (1993)
93216814
JOURNAL
MEDLINE
PUBMED
8096520
COMMENT
Original source text: Homo sapiens (tissue library: lambda Charon 4a) bone marrow DNA.
Location/Qualifiers
1..1327
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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/|cell_type="leukocyte"
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863. .875
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/function="heat shock element"
930. .937
/|gene="PGY1"
/|note="G00-120-712"
/|bound_moiety="unknown"
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931. .938
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/|note="G00-120-712"
980. .990
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/|note="G00-120-712"
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/|note="G00-120-712"
/|number=1

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Bee local similarity 100.0%; Pred. No. 16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCCGCCCGCGCGCTG 25
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1002 GTGCTCAGCCCGCCCGCGCGCTG 978

RESULT 13
AR080193 1688 bp DNA linear PAT 31-AUG-2000
LOCUS AR080193/c
DEFINITION Sequence 2 from patent US 5968735.
ACCESSION AR080193
VERSION AR080193.1 GI:1006928
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1688)
AUTHORS Stein,U. and Walcher,W.
TITLE Vector for the expression of therapy-relevant genes
JOURNAL Patent: US 5968735-A 2 19-OCT-1999;
FEATURES
location/Qualifiers
1..1688
/organism="unknown"
/mol_type="unassigned DNA"

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Best Local Similarity	100.0%;	Pred. No. 15;		
Matches 25;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	GTGCTCAGCCCGCCCGGCGCTG 25		
Db	1534	GTGCTCAGCCCGCCCGGCGCTG 1510		
RESULT 14				
LOCUS	AR080192/c	2090 bp.	DNA	linear
DEFINITION	Sequence 1 from patent US 5968735.			PAT 31-AUG-2000
ACCESSION	AR080192			
VERSION	AR080192.1	GI:10006927		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 2090)			
TITLE	Stein, U. and Walther, W.			
JOURNAL	Vector for the expression of therapy-relevant genes			
FEATURES	Parent: US 5968735-A 1 19-OCT-1999;			
source	1..2090			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
ORIGIN				
Query Match	100.0%;	Score 25;	DB 6;	Length 2090;
Best Local Similarity	100.0%;	Pred. NO. 15;		
Matches 25;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	GTGCTCAGCCCGCCCGGCGCTG 25		
Db	1936	GTGCTCAGCCCGCCCGGCGCTG 1912		
RESULT 15				
LOCUS	A38669/c	2117 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO9411522.			PAT 11-NOV-1999
ACCESSION	A38669			
VERSION	A38669.1	GI:2295152		
KEYWORDS				
SOURCE	Homio sapiens (human)			
ORGANISM	Homio sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
TITLE	1 (bases 1 to 2117)			
JOURNAL	Stein, U. and Walther, W.			
COMMENT	VECTOR FOR THE EXPRESSION OF THERAPY-RELEVANT GENES			
FEATURES	Parent: WO 941152-A 1 26-MAY-1994;			
	MAX DELBRUECK CT FUER MOLEKULA (DE)			
	Other publication DE 428778 940519.			
	Location/Qualifiers			
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	/db_xref="taxon:9606"			
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Best Local Similarity	100.0%;	Pred. No. 15;		

Matches	25;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GTGCTCAGCCCGCCCGGCGCTG	25						
Db	1936	GTGCTCAGCCCGCCCGGCGCTG	1912						

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 Job time : 482.178 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 78.592 Seconds
(without alignments)
520.498 Million cell updates/sec

Title: US-10-007-255-10
Perfect score: 1 gtcgcagccacgccccgcgctg 25
Sequence: 1 gtcgcagccacgccccgcgctg 25

Scoring table: IDENTITY NUC
Gapop 10-0, Gapex 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents, NA.*
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/6C.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/6D.COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	25	100.0	568	2	US-08-439-814-4
4	25	100.0	1318	2	US-08-439-814-3
5	25	100.0	1688	2	US-08-439-814-2
6	25	100.0	2090	2	US-08-439-814-1
7	25	100.0	4646	1	US-08-181-471-2
8	25	100.0	4646	4	US-09-023-655-1167
9	25	100.0	4669	2	US-08-583-276-18
10	25	100.0	4669	6	5206352-3
11	25	100.0	4669	6	5206352-3
12	23.4	93.6	4669	2	US-08-752-447-1
13	23.4	93.6	4669	3	US-09-316-167-1
14	23.4	93.6	4669	4	US-09-397-233-1
15	20	80.0	20	1	US-08-487-1418-2
16	20	80.0	20	1	US-08-927-561-2
17	20	80.0	20	5	PCT-US96-09388-2
18	19.4	77.6	951	4	US-09-902-540-5524
19	19.4	77.6	951	4	US-09-902-540-1266
20	18.8	75.2	18195	4	US-09-902-540-1179
21	18.6	74.4	342	4	US-09-513-999C-13841
22	18.6	74.4	601	4	US-09-949-016-174342
23	18.6	74.4	601	4	US-09-949-016-174534
24	18.6	74.4	41171	4	US-08-311-731A-122
25	18.6	74.4	126337	4	US-09-949-016-16674
26	18.6	74.4	126337	4	US-09-949-016-16675
27	18.2	72.8	388	1	US-07-626-618A-1

28	18.2	72.8	388	1	US-07-928-611-1	Sequence 1, Appl
29	18.2	72.8	388	2	US-08-333-977-1	Sequence 1, Appl
30	18.2	72.8	388	2	US-08-487-811A-1	Sequence 1, Appl
31	18.2	72.8	388	3	US-09-060-694-1	Sequence 1, Appl
32	18.2	72.8	388	3	US-09-378-074-1	Sequence 1, Appl
33	18.2	72.8	388	5	PCT-US93-07370-1	Sequence 1, Appl
34	18.2	72.8	1367	4	US-08-475-742-3	Sequence 3, Appl
35	18.2	72.8	1367	4	US-08-261-293-3	Sequence 3, Appl
36	18.2	72.8	1370	1	US-08-056-051-1	Sequence 1, Appl
37	18.2	72.8	1370	1	US-07-928-611-17	Sequence 1, Appl
38	18.2	72.8	1370	2	US-08-487-811A-17	Sequence 1, Appl
39	18.2	72.8	1370	3	US-09-060-694-17	Sequence 1, Appl
40	18.2	72.8	1370	3	US-09-378-074-17	Sequence 1, Appl
41	18.2	72.8	1370	5	PCT-US93-07370-17	Sequence 1, Appl
42	18.2	72.8	1466	1	US-08-056-051-3	Sequence 3, Appl
43	18.2	72.8	1466	1	US-07-928-611-19	Sequence 19, Appl
44	18.2	72.8	1466	2	US-08-487-811A-19	Sequence 19, Appl
45	18.2	72.8	1466	3	US-09-060-694-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-439-814-5/c
Sequence 5, Application US/08439814
Patent No. 5968735
GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
STREET: Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439, 814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (ERO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE93/01086

FILED DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-439-814-5

Query Match 100.0%; Score 25; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTCAGCCCGCCCGGCGCTG 25
Db 170 GTGCTCAGCCCGCCCGGCGCTG 146

RESULT 2

US-08-439-814-6/c
Sequence 6, Application US/08439814
Patent No. 5968735
GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 6:
LENGTH: 351 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-439-814-6

Query Match 100.0%; Score 25; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTCAGCCCGCCCGGCGCTG 25
Db 170 GTGCTCAGCCCGCCCGGCGCTG 146

RESULT 3

US-08-439-814-4/c
Sequence 4, Application US/08439814
Patent No. 5968735
GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 4:
LENGTH: 568 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-439-814-4

Query Match 100.0%; Score 25; DB 2; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCGAGCCCGGCGCTG 25
DB 414 GTGCTAGCCCGAGCCCGGCGCTG 390

RESULT 4

US-08-439-814-3/C
Sequence 3, Application US/08439814

Patent No. 5968735
GENERAL INFORMATION:

APPLICANT: STEIN, Ulrike
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF

TITLE OF INVENTION: THERAPY-RELEVANT GENES
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI, MARMELSTEIN, MURRAY & ORAM LLP

STREET: 655 Fifteenth Street, N. W., Suite 330 G
CITY: Washington

STATE: DC
COUNTRY: USA

ZIP: 20005-5701
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439, 814

FILING DATE: 12-MAY-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7

FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.

REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7

FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 1318 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-439-814-3

Query Match 100.0%; Score 25; DB 2; Length 1318;
Best Local Similarity 100.0%; Pred. No. 0.87;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCGAGCCCGGCGCTG 25
DB 1164 GTGCTAGCCCGAGCCCGGCGCTG 1140

RESULT 5

US-08-439-814-2/C
Sequence 2, Application US/08439814

Patent No. 5968735
GENERAL INFORMATION:

APPLICANT: STEIN, Ulrike
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF

TITLE OF INVENTION: THERAPY-RELEVANT GENES
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAI, MARMELSTEIN, MURRAY & ORAM LLP

STREET: 655 Fifteenth Street, N. W., Suite 330 G
CITY: Washington

STATE: DC
COUNTRY: USA

ZIP: 20005-5701
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439, 814

FILING DATE: 12-MAY-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7

FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.

REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7

FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 1688 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-439-814-2

Query Match 100.0%; Score 25; DB 2; Length 1688;
Best Local Similarity 100.0%; Pred. No. 0.86;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCGAGCCCGGCGCTG 25
DB 1164 GTGCTAGCCCGAGCCCGGCGCTG 1140

Db 1534 GTGCTCAGCCACGCCCGCGCGCTG 1510

RESULT 6

US-08-439-814-1/c
Sequence 1, Application US/08439814
Patent No. 5968735
GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARWELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439, 814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2090 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-439-814-1

Query Match 100.0%; Score 25; DB 2; Length 2090;

Best Local Similarity 100.0%; Pred. No. 0.85; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1936 GTGCTCAGCCACGCCCGCGCGCTG 1912

RESULT 7

US-08-181-471-2/c

Sequence 2, Application US/08181471
Patent No. 5641508
GENERAL INFORMATION:
APPLICANT: Li, Lingna
APPLICANT: Lishko, Valeryi K.
TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas Fitting
STREET: 12526 High Bluff Drive, Suite 300
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92130
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,471
FILING DATE: 13-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,553
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: ANT0029P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-792-3680
TELEFAX: 619-792-8477
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4267
US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;

Best Local Similarity 100.0%; Pred. No. 0.82; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 251 GTGCTCAGCCACGCCCGCGCGCTG 227

RESULT 8

US-09-023-655-1167/c
Sequence 1167, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cooke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO

STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: word perfect 6.1 for windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1167:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187468
US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCCGCCCGCGGCGCTG 25
|||||
DB 251 GTGCTCAGCCCGCCCGCGGCGCTG 227

RESULT 9
US-08-583-276-18/c
Sequence 18, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
APPLICANT: McDonagh, Kevin T.
APPLICANT: Menhulle, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Carella, Byrne, Bain, Gillfillan,
ADDRESSER: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994
APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 bases
TYPE: nucleic acid
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: Genomic DNA
US-08-583-276-18

Query Match 100.0%; Score 25; DB 2; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCCGCCCGCGGCGCTG 25
|||||
DB 251 GTGCTCAGCCCGCCCGCGGCGCTG 227

RESULT 10
5206352-3/c
Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
;SEQ ID NO:3;
;LENGTH: 4669
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCCGCCCGCGGCGCTG 25
|||||
DB 251 GTGCTCAGCCCGCCCGCGGCGCTG 227

RESULT 11
5206352-3/c
Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
;SEQ ID NO:3;
;LENGTH: 4669
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;

Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCAAGCCCGGCGCTG 25
Db 251 GTGCTAGCCCAAGCCCGGCGCTG 227

RESULT 12

US-08-752-447-1/c
Sequence 1, Application US/08752447
Patent No. 5894088
GENERAL INFORMATION:
APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,447
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: No. 5994088nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669

US-08-752-447-1

Query Match 93.6%; Score 23.4; DB 2; Length 4669;
Best Local Similarity 96.0%; Pred. No. 3.3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCAAGCCCGGCGCTG 25
Db 251 GCGCTAGCCCAAGCCCGGCGCTG 227

RESULT 13
US-09-316-167-1/c
Sequence 1, Application US/09316167
Patent No. 6365357
GENERAL INFORMATION:

APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316,167
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,447
FILING DATE: 15-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: No. 6365357nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669

US-09-316-167-1

Query Match 93.6%; Score 23.4; DB 3; Length 4669;
Best Local Similarity 96.0%; Pred. No. 3.3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCAAGCCCGGCGCTG 25
Db 251 GCGCTAGCCCAAGCCCGGCGCTG 227

RESULT 14

US-09-397-233-1/c
Sequence 1, Application US/09397233
Patent No. 6630327
GENERAL INFORMATION:
APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,233
FILING DATE: 16-Sep-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6630327nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-397-233-1
Query Match 93.6%; Score 23.4; DB 4; Length 4669;
Best Local Similarity 96.0%; Pred. No. 3.3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGCTCAGCCCAAGCGGCGTG 25
DB 251 GCGCTCAGCCCAAGCGGCGTG 227
RESULT 15
US-08-487-141B-2
Sequence 2, Application US/08487141B
Patent No. 5683987
GENERAL INFORMATION:
APPLICANT: Smith, Larry J.
TITLE OF INVENTION: Therapeutic Oligonucleotides
TITLE OF INVENTION: Targeting the Human MDR1 and MRP Genes
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,141B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,180

FILING DATE: 12-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 63082C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215)563-4100
TELEFAX: (215)563-4044
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-487-141B-2
Query Match 80.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTCAGCCCAAGCGGCGG 20
DB 1 GTGCTCAGCCCAAGCGGCGG 20
Search completed: February 9, 2005, 17:11:14
Job time : 79.592 secs

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Sequence 31, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(2307)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-31
```

```
Query Match 100.0%; Score 25; DB 9; Length 2307;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GTGCTCAGCCCGCCCGCGCGCTG 25
DB 251 GTGCTCAGCCCGCCCGCGCGCTG 227
```

```
RESULT 3
US-10-473-126-37/c
; Sequence 37, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 37
; LENGTH: 2932
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-473-126-37
```

```
Query Match 100.0%; Score 25; DB 18; Length 2932;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GTGCTCAGCCCGCCCGCGCGCTG 25
DB 1039 GTGCTCAGCCCGCCCGCGCGCTG 1015
```

```
RESULT 4
US-09-805-020-30/c
; Sequence 30, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: misc feature
; LOCATION: (1)..(4533)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-30
```

```
Query Match 100.0%; Score 25; DB 9; Length 4533;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GTGCTCAGCCCGCCCGCGCGCTG 25
DB 251 GTGCTCAGCCCGCCCGCGCGCTG 227
```

```
RESULT 5
US-10-072-621-2/c
; Sequence 2, Application US/10072621
; Publication No. US20020169137A1
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Conroy, Bruce P.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
; TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY
; FILE REFERENCE: 100103,402
; CURRENT APPLICATION NUMBER: US/10/072,621
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-621-2
```

```
Query Match 100.0%; Score 25; DB 13; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTGCTCAGCCCGCCCGCGCGCTG 25
DB 251 GTGCTCAGCCCGCCCGCGCGCTG 227
```

```
RESULT 6
US-10-097-340-1/c
; Sequence 1, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
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; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-097-340-1

Query Match          100.0%; Score 25; DB 14; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGCTCAGCCCGCCCGGGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGGGCGCTG 227

RESULT 7
US-10-007-926A-258/c
; Sequence 258, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOUJAGATE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: acp-binding cassette, sub-family b
; OTHER INFORMATION: (mdr/cap), member 1 (ABCB1) gene.
; US-10-007-926A-258

Query Match          100.0%; Score 25; DB 15; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGCTCAGCCCGCCCGGGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGGGCGCTG 227

RESULT 8
US-09-968-007A-459/c
; Sequence 459, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
```

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; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 459
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-968-007A-459

Query Match          100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGCTCAGCCCGCCCGGGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGGGCGCTG 227

RESULT 9
US-09-968-007A-747/c
; Sequence 747, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 747
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-968-007A-747

Query Match          100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGCTCAGCCCGCCCGGGCGCTG 25
Db      251 GTGCTCAGCCCGCCCGGGCGCTG 227
```

RESULT 10
US-10-641-643-1167/c
; Sequence 1167, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0855
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4646 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9187468
; SEQUENCE DESCRIPTION: SEQ ID NO: 1167 :
US-10-641-643-1167
Query Match 100.0%; Score 25; DB 17; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTAGCCCAAGCCCGGCGCTG 25
DB 251 GTGCTAGCCCAAGCCCGGCGCTG 227
RESULT 11
US-10-343-657-1/c
; Sequence 1, Application US/10343657
; Publication No. US2004008682A1
; GENERAL INFORMATION:
; APPLICANT: Roninson, Igor B.
; APPLICANT: Ruth, Adam
; TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that improve its
; TITLE OF INVENTION: Ability to confer Resistance to Chemotherapeutic Drugs
; FILE REFERENCE: 00,616-A
; CURRENT APPLICATION NUMBER: US/10/343,657
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/222,313
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (425)..(4264)
US-10-343-657-1
Query Match 100.0%; Score 25; DB 17; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTAGCCCAAGCCCGGCGCTG 25
DB 251 GTGCTAGCCCAAGCCCGGCGCTG 227
RESULT 12
US-10-775-169-198/c
; Sequence 198, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dornier, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-198
Query Match 100.0%; Score 25; DB 18; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTAGCCCAAGCCCGGCGCTG 25
DB 251 GTGCTAGCCCAAGCCCGGCGCTG 227
RESULT 13
US-10-680-516-1/c
; Sequence 1, Application US/10680516
; Publication No. US20040166110A1
; GENERAL INFORMATION:
; APPLICANT: Mecheater, Eugene
; Roninson, Igor B
; TITLE OF INVENTION: Methods and Reagents for Preparing and
; Using Immunological Agents Specific for P-glycoprotein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:


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      APPLICATION NUMBER: US/10/680,516
      FILING DATE: 07-Oct-2003
      CLASSIFICATION: 435
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/752,447
      FILING DATE: 15-NOV-1996
      ATTORNEY/AGENT INFORMATION:
      NAME: Noonan, Kevin E
      REGISTRATION NUMBER: 35,303
      REFERENCE/DOCKET NUMBER: 95,1121
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 312-913-0001
      TELEFAX: 312-913-9808
      INFORMATION FOR SEQ ID NO: 1:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 4669 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: CDNA
      FEATURE:
      NAME/KEY: 5'UTR
      LOCATION: 1..424
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 425..4264
      FEATURE:
      NAME/KEY: 3'UTR
      LOCATION: 4265..4669
      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-680-516-1

Query Match      93.6%; Score 23.4; DB 18; Length 4669;
Best Local Similarity 96.0%; Pred. No. 0.65;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTGCTAGCCAGCCCGCGGCGCTG 25
      |||||
Db      251 GCGCTAGCCAGCCAGCCCGCGGCGCTG 227

RESULT 14
US-09-880-107-3828/c
; Sequence 3828, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-MO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3828
; LENGTH: 2692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X94563
US-09-880-107-3828

Query Match      76.8%; Score 19.2; DB 9; Length 2692;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GTGCTAGCCAGCCCGCGGCGCT 24
```

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      |||||
Db      1083 GTGCCAGCCCGCGCGGCGGCT 1060

RESULT 15
US-09-968-007A-755/c
; Sequence 755, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signal
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 755
; LENGTH: 2692
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-755

Query Match      76.8%; Score 19.2; DB 11; Length 2692;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GTGCTAGCCAGCCCGCGGCGCT 24
      |||||
Db      1083 GTGCCAGCCCGCGCGGCGGCT 1060

Search completed: February 9, 2005, 22:26:36
Job time : 267.667 secs
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PS Example 2; Page 12; 92pp; English.
 XX
 CC The invention relates to a method of treating a subject having or at risk
 CC of developing a haematologic malignancy or multidrug resistance (MDR).
 CC The method involves administering hypoxia inducible factor-1 (HIF-1)
 CC binding molecules or small ubiquitin-like modifier (SUMO)-1 binding
 CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive
 CC element (HRE) binding molecules or antisense nucleic acid molecules and
 CC SUMO-1 binding molecules or antisense molecules are useful for treating a
 CC subject having or at risk of developing haematologic malignancy or MDR
 CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
 CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
 CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
 CC disorders include chronic or acute myeloid leukaemia, e.g. angioleukemia
 CC myeloid metaplasia, essential thrombocythemia or polycythemia vera. The
 CC invention is used in gene therapy. The present sequence is human mdr1
 CC gene HIF-1 binding site DNA
 CC
 SQ Sequence 25 BP; 3 A; 8 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.3; Mismatches 0; Gaps 0;
 Matches 25; Conservative 0; Indels 0; Gaps 0;
 Qy 1 GTGCTCAGCCCAAGCCCGCGCTG 25
 Db 25 GTGCTCAGCCCAAGCCCGCGCTG 1
 RESULT 2
 AAD38999
 ID AAD38999 standard; DNA; 25 BP.
 AC AAD38999;
 DT 23-SEP-2002 (first entry)
 XX
 DE Human mdr1-HRE antisense oligonucleotide #2.
 XX
 KW Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;
 KW hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;
 KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
 KW myeloid disorder; lymphocytic leukaemia; thrombocythemia; myeloma;
 KW angioleukemia; myeloid metaplasia; myeloid leukaemia; gene therapy;
 KW polycythemia vera; hypoxia responsive element; HRE; antisense;
 KW phosphorothioate backbone; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..25
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone"
 FT
 XX
 PN WO200234291-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 25-OCT-2001; 2001WO-US049856.
 XX
 PR 26-OCT-2000; 2000US-0243542P.
 XX
 PA (BGMH) BRIGHAM & WOMENS HOSPITAL INC.
 XX
 PI Colgan SB;
 XX
 DR WPI; 2002-471427/50.
 XX
 PT Treating a subject (at risk of) having a hematologic malignancy or
 PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia
 PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

PT binding molecules.
 XX
 PS Claim 14; Page 43; 92pp; English.
 XX
 CC The invention relates to a method of treating a subject having or at risk
 CC of developing a haematologic malignancy or multidrug resistance (MDR).
 CC The method involves administering hypoxia inducible factor-1 (HIF-1)
 CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
 CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive
 CC element (HRE) binding molecules or antisense nucleic acid molecules and
 CC SUMO-1 binding molecules or antisense molecules are useful for treating a
 CC subject having or at risk of developing haematologic malignancy or MDR
 CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
 CC include lymphocytic leukemia or chronic lymphoproliferative disorders
 CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
 CC disorders include chronic or acute myeloid leukaemia, e.g. angioleukemia
 CC myeloid metaplasia, essential thrombocythemia or polycythemia vera. The
 CC invention is used in gene therapy. The present sequence is an antisense
 CC oligo targeted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its
 CC expression. This oligo is used in the exemplification of the invention
 CC
 SQ Sequence 25 BP; 2 A; 12 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.3; Mismatches 0; Gaps 0;
 Matches 25; Conservative 0; Indels 0; Gaps 0;
 Qy 1 GTGCTCAGCCCAAGCCCGCGCTG 25
 Db 1 GTGCTCAGCCCAAGCCCGCGCTG 25
 RESULT 3
 ABV75271
 ID ABV75271 standard; DNA; 52 BP.
 AC ABV75271;
 DT 07-MAR-2003 (first entry)
 XX
 DE hMDR1 promoter element containing antisense oligonucleotide.
 XX
 KW Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;
 KW immediate early gene; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO200279470-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 29-MAR-2002; 2002MO-US009882.
 XX
 PR 30-MAR-2001; 2001US-0280211P.
 XX
 PA (KING/) KING A C.
 XX
 PI King AC;
 XX
 DR WPI; 2003-103274/09.
 XX
 PT New promoter chimera useful for in vivo or in vitro expression comprises
 PT viral promoter, intron or other transcription regulatory elements and
 PT disease-specific promoter, intron or other transcription regulatory
 PT sequences.
 XX
 PS Example 1; Page 20; 48pp; English.
 XX
 CC The invention relates to a new promoter chimera for in vivo or in vitro
 CC expression that comprises: (a) a viral promoter, intron or other unit
 CC transcription regulatory sequence of any length; and (b) a unit disease-
 CC specific promoter, intron or other unit transcription regulatory sequence
 CC of any length sensitive to genotoxic stress. The promoter chimera, and

vector comprising the chimera are useful for in vivo or in vitro expression. The method is useful for the generation of improved expression constructs for in vitro and in vivo expression of therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter chimera of the present invention are more potent than either promoter standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA element and deletion of HCMV IE sequences not contributing to the activity of promoter chimera

Sequence 52 BP; 7 A; 25 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTAGCCAGCCCGCGCTG 25
3 GTGCTAGCCAGCCCGCGCTG 27

RESULT 4

ABV75270/c
ID ABV75270 standard; DNA; 52 BP.

ABV75270;

07-MAR-2003 (first entry)

hMDR1 promoter element containing sense oligonucleotide.

Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;

Immediate early gene; gene therapy; ss.

Synthetic.

WO200279470-A1.

10-OCT-2002.

29-MAR-2002; 2002WO-US009882.

30-MAR-2001; 2001US-0280211P.

(KING/) KING A C.

KING AC;

WPI; 2003-103274/09.

New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory sequences.

Example 1; Page 20; 48bp; English.

The invention relates to a new promoter chimera for in vivo or in vitro expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-specific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimera, and vector comprising the chimera are useful for in vivo or in vitro expression. The method is useful for the generation of improved therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter chimera of the present invention are more potent than either promoter standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA element and deletion of HCMV IE sequences not contributing to the activity of promoter chimera

Sequence 52 BP; 9 A; 11 C; 25 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTAGCCAGCCCGCGCTG 25
50 GTGCTAGCCAGCCCGCGCTG 26

RESULT 5

ABV75282/c
ID ABV75282 standard; DNA; 56 BP.

ABV75282;

07-MAR-2003 (first entry)

C3 dimer and trimer constructs creating sense oligonucleotide.

Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;

Immediate early gene; gene therapy; ss.

Synthetic.

WO200279470-A1.

10-OCT-2002.

29-MAR-2002; 2002WO-US009882.

30-MAR-2001; 2001US-0280211P.

(KING/) KING A C.

KING AC;

WPI; 2003-103274/09.

New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory sequences.

Example 1; Page 21; 48bp; English.

The invention relates to a new promoter chimera for in vivo or in vitro expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-specific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimera, and vector comprising the chimera are useful for in vivo or in vitro expression. The method is useful for the generation of improved therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter chimera of the present invention are more potent than either promoter standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA element and deletion of HCMV IE sequences not contributing to the activity of promoter chimera

Sequence 56 BP; 10 A; 11 C; 27 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTAGCCAGCCCGCGCTG 25
51 GTGCTAGCCAGCCCGCGCTG 27

RESULT 6

```

ABV75276/c
ID ABV75276 standard; DNA; 56 BP.
XX
AC ABV75276;
XX
DT 07-MAR-2003 (first entry)
XX
DE C3mut3 construct creating sense oligonucleotide.
XX
KW Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;
KM immediate early gene; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO200279470-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009882.
XX
PR 30-MAR-2001; 2001US-0280211P.
XX
PA (KING/) KING A C.
XX
PI King AC;
XX
DR WPI; 2003-103274/09.
XX
PT New promoter chimera useful for in vivo or in vitro expression comprises
PT viral promoter, intron or other transcription regulatory elements and
PT disease-specific promoter, intron or other transcription regulatory
PT sequences.
XX
PS Example 1; Page 21; 48pp; English.
XX
CC The invention relates to a new promoter chimera for in vivo or in vitro
CC expression that comprises: (a) a viral promoter, intron or other unit
CC transcription regulatory sequence of any length; and (b) a unit disease-
CC specific promoter, intron or other unit transcription regulatory sequence
CC of any length sensitive to genotoxic stress. The promoter chimera, and
CC vector comprising the chimera are useful for in vivo or in vitro
CC expression. The method is useful for the generation of improved
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter
CC chimeras of the present invention are more potent than either promoter
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in
CC the construction of promoter chimeras having hMDR1 disease specific DNA
CC element and deletion of HCMV IE sequences not contributing to the
CC activity of promoter chimera
XX
SQ Sequence 56 BP; 10 A; 11 C; 27 G; 8 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTGCTCAGCCACGCCCGCGCTG 25
DB 51 GTGCTCAGCCACGCCCGCGCTG 27

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XX
OS Synthetic.
XX
PN WO200279470-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009882.
XX
PR 30-MAR-2001; 2001US-0280211P.
XX
PA (KING/) KING A C.
XX
PI King AC;
XX
DR WPI; 2003-103274/09.
XX
PT New promoter chimera useful for in vivo or in vitro expression comprises
PT viral promoter, intron or other transcription regulatory elements and
PT disease-specific promoter, intron or other transcription regulatory
PT sequences.
XX
PS Example 1; Page 20; 48pp; English.
XX
CC The invention relates to a new promoter chimera for in vivo or in vitro
CC expression that comprises: (a) a viral promoter, intron or other unit
CC transcription regulatory sequence of any length; and (b) a unit disease-
CC specific promoter, intron or other unit transcription regulatory sequence
CC of any length sensitive to genotoxic stress. The promoter chimera, and
CC vector comprising the chimera are useful for in vivo or in vitro
CC expression. The method is useful for the generation of improved
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter
CC chimeras of the present invention are more potent than either promoter
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in
CC the construction of promoter chimeras having hMDR1 disease specific DNA
CC element and deletion of HCMV IE sequences not contributing to the
CC activity of promoter chimera
XX
SQ Sequence 56 BP; 10 A; 11 C; 27 G; 8 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTGCTCAGCCACGCCCGCGCTG 25
DB 27 GTGCTCAGCCACGCCCGCGCTG 3

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RESULT 7
ABV75272/c
ID ABV75272 standard; DNA; 56 BP.
XX
AC ABV75272;
XX
DT 07-MAR-2003 (first entry)
XX
DE C3mut1 construct creating sense oligonucleotide.
XX
KW Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;
KM immediate early gene; gene therapy; ss.
XX

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RESULT 8
ABV75283
ID ABV75283 standard; DNA; 60 BP.
XX
AC ABV75283;
XX
DT 07-MAR-2003 (first entry)
XX
DE C3 dimer and trimer constructs creating antisense oligonucleotide.
XX
KW Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;
KM immediate early gene; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO200279470-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009882.
XX
PR 30-MAR-2001; 2001US-0280211P.
XX

```

PA (KING/) KING A C.
XX
PI King AC;
XX
DR WPI; 2003-103274/09.
XX
PT New promoter chimera useful for in vivo or in vitro expression comprises
PT viral promoter, intron or other transcription regulatory elements and
PT disease-specific promoter, intron or other transcription regulatory
PT sequences.
XX
PS Example 1; Page 21; 48pp; English.
XX
CC The invention relates to a new promoter chimera for in vivo or in vitro
CC expression that comprises: (a) a viral promoter, intron or other unit
CC transcription regulatory sequence of any length; and (b) a unit disease-
CC specific promoter, intron or other unit transcription regulatory sequence
CC of any length sensitive to genotoxic stress. The promoter chimera, and
CC vector comprising the chimera are useful for in vivo or in vitro
CC expression. The method is useful for the generation of improved
CC expression constructs for in vitro and in vivo expression of
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter
CC chimeras of the present invention are more potent than either promoter
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in
CC the construction of promoter chimeras having hMDR1 disease specific DNA
CC element and deletion of HCMV IE sequences not contributing to the
CC activity of promoter chimera
XX
SQ Sequence 60 BP; 9 A; 28 C; 12 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCACGCCCGCGGCTG 25
DB 6 GTGCTCAGCCACGCCCGCGGCTG 30

RESULT 9
ABV75277
ID ABV75277 standard; DNA; 60 BP.
XX
AC ABV75277;
XX
DT 07-MAR-2003 (first entry)
XX
DE Cmut3 construct creating antisense oligonucleotide.
XX
KW Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;
KW immediate early gene; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO200279470-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009882.
XX
PR 30-MAR-2001; 2001US-0280211P.
XX
PA (KING/) KING A C.
XX
PI King AC;
XX
DR WPI; 2003-103274/09.
XX
PT New promoter chimera useful for in vivo or in vitro expression comprises
PT viral promoter, intron or other transcription regulatory elements and
PT disease-specific promoter, intron or other transcription regulatory
PT sequences.
XX

PS Example 1; Page 21; 48pp; English.
XX
CC The invention relates to a new promoter chimera for in vivo or in vitro
CC expression that comprises: (a) a viral promoter, intron or other unit
CC transcription regulatory sequence of any length; and (b) a unit disease-
CC specific promoter, intron or other unit transcription regulatory sequence
CC of any length sensitive to genotoxic stress. The promoter chimera, and
CC vector comprising the chimera are useful for in vivo or in vitro
CC expression. The method is useful for the generation of improved
CC expression constructs for in vitro and in vivo expression of
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter
CC chimeras of the present invention are more potent than either promoter
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in
CC the construction of promoter chimeras having hMDR1 disease specific DNA
CC element and deletion of HCMV IE sequences not contributing to the
CC activity of promoter chimera
XX
SQ Sequence 60 BP; 9 A; 28 C; 12 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTCAGCCACGCCCGCGGCTG 25
DB 6 GTGCTCAGCCACGCCCGCGGCTG 30

RESULT 10
ABV75273
ID ABV75273 standard; DNA; 60 BP.
XX
AC ABV75273;
XX
DT 07-MAR-2003 (first entry)
XX
DE Cmutl construct creating antisense oligonucleotide.
XX
KW Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1;
KW immediate early gene; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO200279470-A1.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009882.
XX
PR 30-MAR-2001; 2001US-0280211P.
XX
PA (KING/) KING A C.
XX
PI King AC;
XX
DR WPI; 2003-103274/09.
XX
PT New promoter chimera useful for in vivo or in vitro expression comprises
PT viral promoter, intron or other transcription regulatory elements and
PT disease-specific promoter, intron or other transcription regulatory
PT sequences.
XX
PS Example 1; Page 21; 48pp; English.
XX
CC The invention relates to a new promoter chimera for in vivo or in vitro
CC expression that comprises: (a) a viral promoter, intron or other unit
CC transcription regulatory sequence of any length; and (b) a unit disease-
CC specific promoter, intron or other unit transcription regulatory sequence
CC of any length sensitive to genotoxic stress. The promoter chimera, and
CC vector comprising the chimera are useful for in vivo or in vitro
CC expression. The method is useful for the generation of improved
CC expression constructs for in vitro and in vivo expression of
CC therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter

CC chimeras of the present invention are more potent than either promoter
CC standing alone. Sequences ABV75270-283 represent oligonucleotides used in
CC the construction of promoter chimeras having hMDR1 disease specific DNA
CC element and deletion of HCV IE sequences not contributing to the
CC activity of promoter chimera

XX Sequence 60 BP; 9 A; 28 C; 12 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25
DB 30 GTGCTCAGCCCAAGCCCGGCGCTG 54

RESULT 11

ID ADR12342/c
ADRI2342 standard; DNA; 424 BP.

XX ADR12342;

DT 21-OCT-2004 (first entry)

XX Human P-glycoprotein 5'-untranslated region DNA.

XX 88; cytosstatic; VEGF modulator; angiogenesis inhibitor;
KW UTR-dependent expression; Vascular endothelial growth factor;
KW untranslated region; cancer; angiogenesis.

XX Homo sapiens.

XX MO2004065561-A2.

XX 05-AUG-2004.

XX 21-JAN-2004; 2004WO-US001643.

XX 21-JAN-2003; 2003US-0441637P.

XX (PTCT-) PTC THERAPEUTICS INC.

XX Cao L, Trifillis P;

XX WPI; 2004-571681/55.

XX Identifying modulators of untranslated region-dependent expression of a
PT VEGF gene, useful for treating cancer, comprises contacting a compound
PT with a cell or translation mixture containing a reporter gene linked to a
PT VEGF gene UTR.

XX Example; SEQ ID NO 51; 251pp; English.

XX A method of identifying (M1) a compound that modulates untranslated
CC region-dependent expression of a vascular endothelial growth factor
CC (VEGF) gene comprises contacting a member of a library of compounds with
CC a cell or cell-free translation mixture containing a reporter gene
CC operably linked to an untranslated region (UTR) of the VEGF gene, and
CC detecting expression of the reporter gene. A compound is identified as
CC modulator if the level of expression of the reporter gene in the presence
CC of the compound is altered as compared to that in the absence of the
CC compound or in the presence of a control. Compounds identified by M1 are
CC useful for treating, preventing or ameliorating cancer or its symptoms,
CC and/or for inhibiting angiogenesis. This sequence corresponds to a
CC therapeutic untranslated region used in the invention.

XX Sequence 424 BP; 99 A; 108 C; 111 G; 106 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 13; Length 424;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25
DB 251 GTGCTCAGCCCAAGCCCGGCGCTG 227

RESULT 12

ID AAQ62615/c
AAQ62615 standard; DNA; 568 BP.

XX AAQ62615;

DT 25-MAR-2003 (revised)

DT 17-JAN-1995 (first entry)

DE Human mdr-1 promoter fragment.

XX inducible promoter; cytosstatic agent; adriamycin; vincristine;
KW multiple drug resistance; mdr-1; mammalian expression vector;
KW cancer therapy; 88.

XX Homo sapiens.

XX DE4238778-A1.

XX 19-MAY-1994.

XX 12-NOV-1992; 92DE-04238778.

XX 12-NOV-1992; 92DE-04238778.

XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

XX Stein U, Walther W;

XX WPI; 1994-168680/21.

XX New mammalian expression vector useful for gene therapy, - comprising the
PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to
PT cytosstatic agents.

XX Claim 2; Page 6; 7pp; German.

XX This is a preferred fragment of the mdr-1 gene promoter, isolated from
CC human DNA. The mdr-1 promoter and enhancer elements are inducible by
CC cytosstatic agents such as vincristine and adriamycin which are used in
CC cancer therapy. Vectors comprising the promoter and enhancer sequences
CC operably linked to heterologous genes coding for therapeutic agents are
CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
CC control of cytosstatic agents. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 568 BP; 142 A; 127 C; 143 G; 156 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 568;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25
DB 414 GTGCTCAGCCCAAGCCCGGCGCTG 390

RESULT 13

ID ABX94595/c
ABX94595 standard; DNA; 633 BP.

XX ABX94595;

DT 17-JUN-2003 (first entry)

XX Human Mdr1 DNA SEQ ID 3.

KW Mdr1, cytosine methylation; hydrogen sulphite; diagnosis; dementia;
XX 5-methylcytosine; amplification; prognosis; side effect; medication; bone;
KW cancer; central nervous system disorder; aggression; muscle; endocrine;
XX abnormal development; personality disorder; behavioural disorder; injury;
KW brain damage; psychotic disorder; cardiovascular disease; infection;
KW gastrointestinal tract; sexual malfunction; de.
OS Homo sapiens.
XX WO2003023760-A2.
PN 09-JAN-2003.
XX 27-JUN-2002; 2002WO-DE002433.
XX 27-JUN-2001; 2001DE-01032212.
XX (EPIC-) EPIDENOMICS AG.
XX Discler J, Leu E;
PI WPI; 2003-201513/19.
XX Determining cytosine methylation in a genomic DNA sample by treating with
PT hydrogen sulfite and analyzing the result, to diagnose associated
PT conditions including cancer and brain disorders.
XX Example 1; Page 17; 38pp; German.
XX This invention describes a novel method of determining cytosine
CC methylation in a sample of genomic DNA which comprises treating the
CC sample with hydrogen sulphite so that the cytosine is converted to uracil
CC whilst 5-methylcytosine remains unchanged, amplifying sections of the DNA
CC using at least 2 PCR primers and studying the base composition of both
CC complementary amplified strands whereby methylation status is deduced
CC from the difference in molecular weight of the two strands. The method is
CC used to diagnose and/or prognosis unwanted side effects of medication,
CC cancer, central nervous system disorders, aggression symptoms or
CC behavioural disorders, clinical, psychological and social consequence of
CC brain damage, psychotic and personality disorders, dementia and
CC associated disorders, cardiovascular disease, malfunction, bone or
CC disease of the gastrointestinal tract, breathing system, damage or
CC endocrine or metabolic system, injury, infection, abnormal development or
CC sexual malfunction. This sequence represents the human Mdr1 DNA fragment
CC amplified by the PCR primers represented in ABX94593 & ABX94594 and is
CC used to illustrate the method of the invention
XX
SQ Sequence 633 BP; 161 A; 143 C; 165 G; 164 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 8; Length 633;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25
DB 422 GTGCTCAGCCCAAGCCCGGCGCTG 398
RESULT 14
AB283718/c
ID AB283718 standard; cDNA; 1024 BP.
XX AB283718;
XX 14-MAY-2003 (first entry)
XX Toxicologically relevant human nucleotide sequence #877.
XX Toxicologically relevant gene; toxicological response; gene; ss.
OS Homo sapiens.
XX WO2003016500-A2.
PN

XX 27-FEB-2003.
PD 16-ANG-2002; 2002WO-US026514.
XX 16-AUG-2001; 2001US-0313080P.
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweizer K;
PI Alen P;
XX WPI; 2003-268322/26.
XX Determining a toxicological response to an agent, useful for screening of
PT drugs, comprises comparing the expression profile of one or more human
PT toxic response genes to a reference gene expression profile indicative of
PT toxicity.
XX Claim 1; Page 271; 455pp; English.
XX The present invention describes a method (M1) for determining a
CC toxicological response to an agent, which comprises comparing the
CC expression profile of one or more human toxic response genes to a
CC reference gene expression profile indicative of toxicity, and so
CC determining the presence of a toxic response to the agent. Also
CC described: (1) an array comprising one or more polynucleotides selected
CC from the genes corresponding to the partial sequences given in AB282842
CC to AB284764, or their fragments of at least 20 nucleotides, or homologues
CC; and (2) determining if a gene putatively identified to be a toxic
CC response gene plays a role on toxic response pathways by determining the
CC expression profile of the gene after exposure of cells or a human subject
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC exposing cells to an agent or isolating cells from a human subject who
CC was exposed to an agent; (b) obtaining the test gene expression profile
CC for a putatively identified toxic response gene after exposure to a known
CC toxic pharmaceutical or industrial agent; and (c) comparing the test
CC profile to the expression profile of a gene with a similar function or
CC comparing the test profile to the expression profile of that gene after
CC exposure to other known toxic compounds. The methods are useful for
CC predicting and determining toxicological responses on a cellular, organ
CC or system level. The arrays comprising the human genes are useful for
CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
SQ Sequence 1024 BP; 287 A; 197 C; 260 G; 280 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 10; Length 1024;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GTGCTCAGCCCAAGCCCGGCGCTG 25
DB 251 GTGCTCAGCCCAAGCCCGGCGCTG 227
RESULT 15
AA062614/c
ID AA062614 standard; DNA; 1318 BP.
XX AA062614;
XX 25-MAR-2003 (revised)
XX 17-JAN-1995 (first entry)
XX Human mdr-1 promoter fragment.
XX inducible promoter; cytostatic agent; adriamycin; vincristine;
KW multiple drug resistance; mdr-1; mammalian expression vector;
KW cancer therapy; ss.
XX Homo sapiens.
XX DE4238778-A1.
PN

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XX 19-MAY-1994.
PD 12-NOV-1992; 92DE-04238778.
XX 12-NOV-1992; 92DE-04238778.
PE 12-NOV-1992; 92DE-04238778.
XX 12-NOV-1992; 92DE-04238778.
FR 12-NOV-1992; 92DE-04238778.
XX 12-NOV-1992; 92DE-04238778.
PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
XX (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
PI Stein U, Walther W;
XX WPI; 1994-168680/21.
DR WPI; 1994-168680/21.
XX New mammalian expression vector useful for gene therapy, - comprising the
PT promoter and/or the enhancer of the mdr-1 gene which is susceptible to
PT cytosstatic agents.
XX Claim 2; Page 5; 7pp; German.
PS Claim 2; Page 5; 7pp; German.
XX This is a preferred fragment of the mdr-1 gene promoter, isolated from
CC human DNA. The mdr-1 promoter and enhancer elements are inducible by
CC cytosstatic agents such as vincristine and adriamycin which are used in
CC cancer therapy. Vectors comprising the promoter and enhancer sequences
CC operably linked to heterologous genes coding for therapeutic agents are
CC claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes,
CC interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the
CC control of cytosstatic agents. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX Sequence 1318 BP; 430 A; 237 C; 277 G; 374 T; 0 U; 0 Other;
SQ Sequence 1318 BP; 430 A; 237 C; 277 G; 374 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 1318;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTAGCCGACCCGCGGCTG 25
DB 1164 GTGCTAGCCGACCCGCGGCTG 1140

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Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds
(without alignments)
388.593 Million cell updates/sec

Title: us-10-007-255-10

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Sequence: IDENTITY NUC

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: gb_est2: *
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4: gb_est3: *
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6: gb_est5: *
7: gb_est6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	20.2	80.8	738	BU122038	BU122038
7	20.2	80.8	816	BU287542	BU287542
8	20.2	80.8	929	BU376890	BU376890
9	20.2	80.8	1000	BU845700	BU845700
10	20.2	80.8	1017	BU219968	BU219968
11	20.2	80.8	1440	BC015458	BC015458
12	19.2	76.8	319	AM354719	AM354719
13	19.2	76.8	401	AV663420	AV663420
14	19.2	76.8	452	AV589422	AV589422
15	19.2	76.8	485	CK846580	CK846580
16	19.2	76.8	486	BM445737	BM445737
17	19.2	76.8	488	BT726148	BT726148
18	19.2	76.8	514	BM431190	BM431190
19	19.2	76.8	532	CB423537	CB423537
20	19.2	76.8	535	BE212025	BE212025
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26	19.2	76.8	593	4	BI527608	BI527608
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28	19.2	76.8	623	5	BO809798	BO809798
29	19.2	76.8	632	2	BF045698	BF045698
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31	19.2	76.8	652	4	BG855426	BG855426
32	19.2	76.8	652	4	BG857646	BG857646
33	19.2	76.8	665	4	BI720235	BI720235
34	19.2	76.8	670	5	BO808123	BO808123
35	19.2	76.8	681	7	CK847926	CK847926
36	19.2	76.8	692	4	BG845541	BG845541
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41	18.8	75.2	622	1	AL677976	AL677976
42	18.8	75.2	641	1	AL960041	AL960041
43	18.8	75.2	649	1	AL846843	AL846843
44	18.8	75.2	687	6	CD874424	CD874424
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ALIGNMENTS

RESULT 1
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LOCUS BP218711 Sugano cDNA library, caudate nucleus Homo sapiens CDNA
DEFINITION clone CNR05381, mRNA sequence.
ACCESSION BP218711
VERSION BP218711.1 GI:52091614
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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1..582
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CNR05381"
/tissue_type="caudate nucleus"
/clone_lib="Sugano cDNA library, caudate nucleus"

ORIGIN
Query Match 100.0%; Score 25; DB 5; Length 582;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTACGCCACCGCCCGCGCTG 25
Db 472 GTGCTACGCCACCGCCCGCGCTG 448

RESULT 2
BP348942/c 582 bp mRNA linear EST 17-SEP-2004
LOCUS BP348942 Sugano cDNA library, brain Homo sapiens CDNA clone
DEFINITION SZR02494, mRNA sequence.

ACCESSION	BP348942	BP348942	GI:52278927	
VERSION	EST.			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 582)			
TITLE	Suzuki, Y., Yamaashita, R., Shiroya, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.			
JOURNAL	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions			
COMMENT	Genome Res. 14 (9), 1711-1718 (2004) Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp.			
FEATURES	location/Qualifiers			
source	1..582			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="SZR02494"			
	/tissue_type="brain"			
	/clone_lib="Sugano cDNA library, brain"			
ORIGIN				
Query Match	100.0%;	Score 25;	DB 5;	Length 582;
Best Local Similarity	100.0%;	Pred. No. 22;		
Matches	25;	Conservative 0;	Mismatches 0;	Indels 0;
	Gaps 0;			
Qy	1 GTGCTCAGCCCAAGCCCGCGCGCTG 25			
Db	382 GTGCTCAGCCCAAGCCCGCGCGCTG 358			
RESULT 3				
BB608269/c				
LOCUS				
DEFINITION	BB608269 RIKEN full-length enriched, 2 days pregnant adult female			
ACCESSION	BB608269			
VERSION	BB608269			
KEYWORDS	BB608269.1 GI:11563446			
SOURCE	EST.			
ORGANISM	Mus musculus (house mouse)			
	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 280)			
AUTHORS	Atawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiroaka, T., Hirozane, T., Hodojima, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Kono, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Watahiki, K., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Miyamatsu, M. and Hayashizaki, Y.			
	RIKEN Mouse ESTs (Atawa, K. et al. 2000)			
	Unpublished (2000)			
	Contact: Yoshihide Hayashizaki			
	Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute			
	The Institute of Physical and Chemical Research (RIKEN)			
	1-7-22 Saitama-cho, Tsukuba, Ibaraki, 305-8565, Japan			
	Tel: 81-45-503-9222			
	Fax: 81-45-503-9216			
	Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/			
	Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Miyamatsu, M. and Hayashizaki, Y.			
	Thermolabile esterase and thermolabile esterase			

trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitenmai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.ritc.riken.go.jp>) for
 further details.

Location/Qualifiers
 1..280
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="E23010P14"
 /sex="female"
 /tissue_type="oviduct"
 /dev_stage="2 days pregnant adult"
 /lab_host="MDH10B"
 /clone_lib="RIKEN full-length enriched, 2 days pregnant
 adult female oviduct"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGGAGAGAGCGCGCCGCACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGGAGAGAGATTCGAGTTATTTATTTATTTATTCCTCCCCCCCC 3']. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 80.8%; Score 20.2; DB 2; Length 280;
 Best Local Similarity 88.0%; Pred. No. 1.6e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTGCTCAGCCACGCGCGCGCTG 25
 Db 95 GTGCTCAGCGCGCGCCGCGCGCTG 71

RESULT 4
 CD737438/c 634 bp mRNA linear EST 26-JUN-2003
 LOCUS 40222525 1GAL - Chicken Intestinal Lymphocyte Gallus gallus cDNA
 DEFINITION clone 1GAL_80L16 5', mRNA sequence.
 ACCESSION CD737438
 VERSION CD737438.1 GI:32286287
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 1 (bases 1 to 634)
 Min, W., Lillehoj, H.S., Ashwell, C.M., Matukumalli, L.K., van
 Rassel, C. and Han, J.Y.
 Chicken intestinal lymphocyte EST database as a resource for the
 analysis of mucosal immune function
 Unpublished (2003)
 Contact: Hyun S. Lillehoj
 Animal Parasite Diseases Laboratory
 Animal and Natural Resources Institute, USDA
 Bldg. 1043, BARC-East, Beltsville, MD 20705, USA

REFERENCE
 AUTHORS TITLE
 JOURNAL COMMENT

trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Kitenmai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.ritc.riken.go.jp>) for
 further details.

Location/Qualifiers
 1..280
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="E23010P14"
 /sex="female"
 /tissue_type="oviduct"
 /dev_stage="2 days pregnant adult"
 /lab_host="MDH10B"
 /clone_lib="RIKEN full-length enriched, 2 days pregnant
 adult female oviduct"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGGAGAGAGCGCGCCGCACTCGAGTTTCTTTTCTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGGAGAGAGATTCGAGTTATTTATTTATTTATTCCTCCCCCCCC 3']. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 pBluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 80.8%; Score 20.2; DB 2; Length 280;
 Best Local Similarity 88.0%; Pred. No. 1.6e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTGCTCAGCCACGCGCGCGCTG 25
 Db 95 GTGCTCAGCGCGCGCCGCGCGCTG 71

RESULT 4
 CD737438/c 634 bp mRNA linear EST 26-JUN-2003
 LOCUS 40222525 1GAL - Chicken Intestinal Lymphocyte Gallus gallus cDNA
 DEFINITION clone 1GAL_80L16 5', mRNA sequence.
 ACCESSION CD737438
 VERSION CD737438.1 GI:32286287
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 1 (bases 1 to 634)
 Min, W., Lillehoj, H.S., Ashwell, C.M., Matukumalli, L.K., van
 Rassel, C. and Han, J.Y.
 Chicken intestinal lymphocyte EST database as a resource for the
 analysis of mucosal immune function
 Unpublished (2003)
 Contact: Hyun S. Lillehoj
 Animal Parasite Diseases Laboratory
 Animal and Natural Resources Institute, USDA
 Bldg. 1043, BARC-East, Beltsville, MD 20705, USA

REFERENCE
 AUTHORS TITLE
 JOURNAL COMMENT

Tel: 3015048771
Fax: 3015045103
Email: h1111eh@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt - -trim fasta. Vector identified
by cross match using options -mismatch 12 -mismatch 18
Plate: 80 row: L column: 16
Seq primer: ATTTAGGTGACACTAATG
High quality sequence stop: 634.
Location/Qualifiers

FEATURES

source

1. 634
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn SC"
/db_xref="taxon:9031"
/clone="IGAL.80L16"
/sex="mixed"
/tissue_type="Gut"
/cell_type="lymphocyte"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_1lb="IGAL - Chicken Intestinal Lymphocyte"
/note="Organ: Intestine; Vector: PCMV-SPORT6; Site 1:
Sal; Site 2: NotI; Normalized library from chicken gut
infected with coccidia duodenum and middle gut."

ORIGIN

Query Match 80.8%; Score 20.2; DB 6; Length 634;
Best Local Similarity 88.0%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCCAGCGCGCGCTG 25
|||
557 GTACTCAGCCCGCCTCAGCGCTG 533

RESULT 5
BU382879/c 652 bp mRNA linear EST 28-NOV-2002
LOCUS 60358284FP1 CSEQCHN75 Gallus gallus cDNA clone CHEST534a14 5', mRNA
DEFINITION
SEQUENCE
ACCESSION BU382879
VERSION BU382879.1 GI:25890880
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 652)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers
1. 652
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="CHEST534a14"
/dev_stage="3c"
/lab_host="DH10B"

/clone_1lb="CSEQCHN75"
/note="Organ: trunks; Vector: pbluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pbluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
1996) 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 652;
Best Local Similarity 88.0%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCTAGCCCCAGCGCGCGCTG 25
|||
562 GTACTCAGCCCGCCTCAGCGCTG 538

RESULT 6
BU122038/c 738 bp mRNA linear EST 25-NOV-2002
LOCUS 603147071F1 CSEQCHL17 Gallus gallus cDNA clone CHEST147n17 5', mRNA
DEFINITION
SEQUENCE
ACCESSION BU122038
VERSION BU122038.1 GI:25332165
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 738)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers
1. 738
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST147n17"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="CSEQCHL17"
/note="Organ: kidney + adrenal; Vector: pbluescript II
KS(+); Site 1: EcoRI; Site 2: NotI; Modification of
cDNA produced with the T-trimmed protocol (construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pbluescript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor

containing Bsg1 and BamHI sites
[5'ggccgcgcagcccgatccgaataaaag]
[5'atctcttttttcgacccggcgctgacgcg]

ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 738;
Best Local Similarity 88.0%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GTGCTCAGCCCGCCCGCGCGCTG 25
561 GTACTCAGCCCGCCCGCTCAGCGCTG 537

RESULT 7

BU287542/c 816 bp mRNA linear EST 27-NOV-2002
LOCUS 603608037P1 CSEQCHN55 Gallus gallus CDNA clone CHEST593110 5', mRNA

ACCESSION BU287542
VERSION BU287542.1 GI:25736998
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 816)

REFERENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
AUTHORS Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.,
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392

COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES

source

1..816
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST593110"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN55"
/note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 816;
Best Local Similarity 88.0%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTGCTCAGCCCGCCCGCGCGCTG 25
Db 572 GTACTCAGCCCGCCCGCTCAGCGCTG 548

RESULT 8 929 bp mRNA linear EST 26-NOV-2002
BU376890/c
LOCUS 603812819P1 CSEQCHN74 Gallus gallus CDNA clone CHEST80265 5', mRNA

ACCESSION BU376890
VERSION BU376890.1 GI:25884891
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 929)

REFERENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
AUTHORS Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.,
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392

COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES

source

1..929
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST80265"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN74"
/note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 929;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GTGCTCAGCCCGCCCGCGCGCTG 25
Db 63 GTACTCAGCCCGCCCGCTCAGCGCTG 39

RESULT 9 1000 bp mRNA linear EST 16-OCT-2002
BU845700
LOCUS 6045700
DEFINITION AGENCOURT_10414348 NIH_MGC_109 Homo sapiens cDNA clone

IMAGE:6579377 5', mRNA sequence.
 ACCESSION B0845700
 VERSION B0845700.1 GI:24030141
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1000)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LCM2782 row: 3 column: 17
 High quality sequence start: 14
 High quality sequence stop: 443.
 Location/Qualifiers
 1..1000
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6579377"
 /tissue_type="teratocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_109"
 /note="Organ: ovary; Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 80.8%; Score 20.2; DB 5; Length 1000;
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 GTGCTCAGCCAGCGCCCGGCGCTG 25
 Db 28 GGCGCTGTGCCCCCGCGCGCTG 52
 RESULT 10
 LOCUS B0219968 1017 bp mRNA linear EST 02-MAY-2002
 DEFINITION AGENCOURT 7594073 NIH_MGC_70 Homo sapiens CDNA clone IMAGE:6021580
 5', mRNA sequence.
 ACCESSION B0219968
 VERSION B0219968.1 GI:20401357
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1017)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM13227 row: 1 column: 05
 High quality sequence stop: 425.
 Location/Qualifiers
 1..1017
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6021580"
 /tissue_type="epithelioid carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_70"
 /note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."
 ORIGIN
 Query Match 80.8%; Score 20.2; DB 5; Length 1017;
 Best Local Similarity 88.0%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 GTGCTCAGCCAGCGCCCGGCGCTG 25
 Db 84 GGCGCTGTGCCCCCGCGCGCTG 108
 RESULT 11
 LOCUS BC015458 1440 bp mRNA linear HTC 04-MAR-2003
 DEFINITION BC015458 Homo sapiens clone IMAGE:3456552, mRNA.
 ACCESSION BC015458
 VERSION BC015458.1 GI:21955332
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1440)
 AUTHORS Strauberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: http://www.sngc.stanford.edu
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Series: IPAK Plate: 4 Row: 1 Column: 17
 This clone has the following problem: retained intron.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3456552"
 /tissue_type="Cervix, carcinoma"
 /clone_id="NIH_MGC_12"

ORIGIN /lab host="DH10B"
/note="Vector: pCMV-SPORT6"

Query Match 80.8%; Score 20.2; DB 3; Length 1440;
Best Local Similarity 88.0%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGCTAGCCGCGCCGCGCGCTG 25
Db 210 GGCTCTGCCCCCGCGCGCGCTG 186

RESULT 12
LOCUS AM354719 319 bp mRNA linear EST 25-APR-2001
DEFINITION 36851 MARC 4BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION AM354719
VERSION AM354719.1 GI:6853709
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Smith,T.P.L., Grosse,W.M., Preking,B.A., Roberts,A.J., Stone,R.T.,
1 (bases 1 to 319)
Cassas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pettes,G., Holt,I., Karanycheva,S., Liang,F.,
Quackenbush,J., and Keefe,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE
JOURNAL MEDLINE
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: emitch@meat.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.960904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG
Plate: 9 row: M column: 16
Seq primer: TAATACGACTCACTATGAGG.
Location/Qualifiers
1. .319
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from day 20 and day 40
embryos."

FEATURES
source

ORIGIN

Query Match 76.8%; Score 19.2; DB 2; Length 319;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCTAGCCGCGCCGCGCGCTG 25
Db 313 TGCTAGCCGCGCTGCGCGCTG 290

RESULT 13

AV663420/c 401 bp mRNA linear EST 28-NOV-2001
LOCUS AV663420 Bos taurus brain fetus Bos taurus cDNA clone E1BR036E05
DEFINITION 3', mRNA sequence.

ACCESSION AV663420
VERSION AV663420.1 GI:9922450
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
1 (bases 1 to 401)
Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE 21570554
PUBMED 11713328
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Niishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp

Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1. .401
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone_lib="E1BR036E05"
/tissue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
/clone_lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site 1: SalI; Site 2: NotI; Poly A
was deleted from a NotI site"

ORIGIN

Query Match 76.8%; Score 19.2; DB 1; Length 401;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCTAGCCGCGCCGCGCGCTG 25
Db 284 TGCTAGCCGCGCTGCGCGCTG 261

RESULT 14
LOCUS AV589422/c 452 bp mRNA linear EST 27-NOV-2001
DEFINITION AV589422 Bos taurus brain fetus Bos taurus cDNA clone E1BR006D03
3', mRNA sequence.
ACCESSION AV589422
VERSION AV589422.1 GI:9700415
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
1 (bases 1 to 452)
Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)

MEDLINE
PUBMED
COMMENT

21570554
11713328
Contact: Yoshihazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Oakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazueugi@cocoa.ocn.ne.jp

Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES

source

location/Qualifiers
1..452
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="E1BR006D03"
/tissue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
/clone_id="Bos taurus brain fetus"
/note="Vector: pZ1; Site 1: SalI; Site 2: NotI; Poly A
was deleted from a NotI site"

ORIGIN

Query Match 76.8%; Score 19.2; DB 1; Length 452;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCTACGCCACGCCCGCGCTG 25
|||||

Db 284 TGCTACGCCCTGCGCTGCGCTG 261
|||||

RESULT 15

CK846580/c 485 bp mRNA linear EST 05-MAR-2004
LOCUS 969088 MARC 4BOV Bos taurus cDNA 3', mRNA sequence.
DEFINITION CK846580
ACCESSION CK846580
VERSION CK846580.1 GI:45207234
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 485)

REFERENCE
AUTHORS Smith,T.P.L., Groose,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Cassab,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keefe,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TP,
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smtlth@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.

Plate: 74 row: H column: 8
Seq primer: GTAATACGACTCAGCTATAGGG.

FEATURES

source

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/db_xref="taxon:9913"

/tissue_type="pooled"
/lab_host="DH10B"
/clone_id="MARC 4BOV"
/note="Vector: PCMV SPORTS; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."

ORIGIN

Query Match 76.8%; Score 19.2; DB 7; Length 485;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGCTACGCCACGCCCGCGCTG 25
|||||

Db 315 TGCTACGCCCTGCGCTGCGCTG 292
|||||

Search completed: February 9, 2005, 21:55:34
Job time : 2452.85 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds
(without alignments)
2517.530 Million cell updates/sec

Title: US-10-007-255-11
Perfect score: 1 cccagcatccacgaagcagagtc 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenBml1:
1: gb_da:
2: gb_hcg:
3: gb_in:
4: gb_on:
5: gb_ov:
6: gb_pac:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_by:
13: gb_un:
14: gb_vl:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX504308 Sequence
2	25	100.0	25	6	AX504325 Sequence
3	25	100.0	976	9	HUMMDR1A02
4	25	100.0	976	11	G19985
5	25	100.0	1022	6	AX597862
6	25	100.0	2932	6	CQ806551
7	25	100.0	2932	6	AX457064
8	25	100.0	2932	6	AX598697
9	25	100.0	2932	6	AX767353
10	25	100.0	2932	6	AX795658
11	25	100.0	2932	6	AX822109
12	25	100.0	2932	6	AX825749
13	25	100.0	2932	6	HSMMDR1A
14	25	100.0	177380	6	AX706985
15	25	100.0	177380	6	AX707915
16	25	100.0	177380	5	AC002457
17	19.8	79.2	182128	5	AC147446
18	19.8	79.2	242082	2	AC121699
19	19.8	79.2	261608	2	AC097158

20	19.8	79.2	272301	2	AC133673	AC133673 Rattus no
21	19.8	79.2	349926	1	BX571660	BX571660 Mollusca
22	19.2	76.8	59032	10	BX005046	BX005046 Mouse DNA
23	19.2	76.8	67699	8	AB016815	Continuation (9 of
24	19.2	76.8	96335	10	AC073297	AC073297 Mus muscu
25	19.2	76.8	121813	2	AC147587	AC147587 Ornithoth
26	19.2	76.8	129814	5	AC116614	AC116614 Homo sapi
27	19.2	76.8	130460	5	AC098806	AC098806 Takifugu
28	19.2	76.8	148619	2	AC151162	AC151162 Bos tauru
29	19.2	76.8	151750	9	AC003666	AC003666 Homo sapi
30	19.2	76.8	161194	2	AC139647	AC139647 Rattus no
31	19.2	76.8	179880	4	AC150482	AC150482 Bos tauru
32	19.2	76.8	181004	9	CNS01DTY	AL132990 Human chr
33	19.2	76.8	189228	2	AC151176	AC151176 Bos tauru
34	19.2	76.8	194313	5	BX323807	BX323807 Zebrafish
35	19.2	76.8	198478	2	AC117692	AC117692 Mus muscu
36	19.2	76.8	203839	2	AC091288	AC091288 Mus muscu
37	19.2	76.8	207584	2	AC103892	AC103892 Rattus no
38	19.2	76.8	216892	2	AC123206	AC123206 Rattus no
39	19.2	76.8	221430	2	AC098629	AC098629 Rattus no
40	19.2	76.8	220661	2	AC132770	AC132770 Rattus no
41	19.2	76.8	250495	10	AL844873	AL844873 Mus muscu
42	19.2	76.8	250600	2	AC115307	AC115307 Rattus no
43	19.2	76.8	300350	1	AP006574	AP006574 Gloeobact
44	19.2	76.8	346542	2	AC120727	AC120727 Rattus no
45	19.2	76.8	346542	2	AC120727	AC120727 Rattus no

ALIGNMENTS

RESULT 1	AX504308	Sequence 11 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504308					
DEFINITION	AX504308					
ACCESSION	AX504308.1	GI:23366126				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE	1	Colgan, S.P.				
AUTHORS		Compositions and methods for treating hematologic malignancies and				
TITLE		multiple drug resistance				
JOURNAL		Patent: WO 0234291-A 11 02-MAY-2002;				
FEATURES		THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)				
source		location/Qualifiers				
ORIGIN		1..25				
Query Match		/organism="Homo sapiens"				
Best Local Similarity		/mol_type="unassigned DNA"				
Matches	25; Conservative	/db_xref="taxon:9606"				
QY	1	CCAGCATCTCCACGAAGCAGAGTT 25				
Db	1	CCAGCATCTCCACGAAGCAGAGTT 25				
RESULT 2	AX504325/c	Sequence 28 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504325					
DEFINITION	AX504325					
ACCESSION	AX504325.1	GI:23386137				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1
 Colgan, S.P.
 Compositiions and methods for treating hematologic malignancies and
 multiple drug resistance
 Patent: WO 0234291-A 28 02-MAY-2002;
 THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
 Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
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 Best Local Similarity 100.0%; Pred. No. 0.67;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CCAGCATCTCCAGAGGAGGAGTT 25
 25 CCAGCATCTCCAGAGGAGGAGTT 1
 Db
 25 CCAGCATCTCCAGAGGAGGAGTT 1
 RESULT 3
 HUMMDRIA02/c 976 bp DNA linear PRI 08-JAN-1995
 LOCUS
 DEFINITION Human P-glycoprotein (MDR1) gene, 5' flank.
 ACCESSION M29423.1 J05168 M18754
 VERSION M29423.1 GI:187472
 KEYWORDS P-glycoprotein; multidrug resistance.
 SEGMENT 2 of 26
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 976)
 Ueda, K., Pastan, I. and Gottesman, M.M.
 Isolation and sequence of the promoter region of the human
 multidrug-resistance (P-glycoprotein) gene
 J. Biol. Chem. 262 (36), 17432-17436 (1987)
 JOURNAL MEDLINE 86087023
 PUBMED 2891692
 REFERENCE 2 (bases 1 to 976)
 Chen, C.J., Clark, D., Ueda, K., Pastan, I., Gottesman, M.M. and
 Roninson, I.B.
 Genomic organization of the human multidrug resistance (MDR1) gene
 and origin of P-glycoproteins
 J. Biol. Chem. 265 (1), 506-514 (1990)
 JOURNAL MEDLINE 90094448
 PUBMED
 COMMENT Original source text: Human multidrug resistant cell line KB-V1
 DNA.
 [2] revises [1].
 Draft entry and computer-readable sequence for [1] kindly submitted
 by I.B.Roninson, 27-OCT-1989.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="7q21"
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 /note="PGY1 mRNA and intron (alt.); G00-120-712"
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 <1..244
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 /note="PGY1, intron A"
 prim_transcript 435..>976
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 intron
 569..>976
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 /note="PGY1"

/note="PGY1, intron A"
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 Query Match 100.0%; Score 25; DB 9; Length 976;
 Best Local Similarity 100.0%; Pred. No. 0.61;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CCAGCATCTCCAGAGGAGGAGTT 25
 947 CCAGCATCTCCAGAGGAGGAGTT 923
 Db
 947 CCAGCATCTCCAGAGGAGGAGTT 923
 RESULT 4
 G19985/c 976 bp DNA linear STS 28-SEP-1998
 LOCUS
 DEFINITION SMSST10 Eric D. Green Homo sapiens STS genomic, sequence tagged
 site.
 ACCESSION G19985
 VERSION G19985.1 GI:1254684
 KEYWORDS STS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 976)
 Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F.,
 Weintrub, L.A., Mohr, T.L., R.M., Peluso, D.C., Fulton, R.S.,
 Leckie, M.P. and Green, E.D.
 A collection of 1814 human chromosome 7-specific STS
 Genome Res. 7 (1), 59-64 (1997)
 JOURNAL MEDLINE 97189344
 PUBMED 9037602
 REFERENCE 2 (bases 1 to 976)
 Green, E.D.
 Human chromosome 7 STSs (1997)
 Unpublished (1997)
 JOURNAL
 TITLES
 JOURNAL
 COMMENT
 Synonyms: PGY1
 GDB: D8B:583426
 GDB: D8B:583426
 GDB: D8B:583426
 GDB: D8B:583426
 Contact: Eric D. Green
 Genome Technology Branch
 National Human Genome Research Institute/NIH
 49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
 Tel: 3014020201
 Fax: 3014024735
 Email: egreen@nhgri.nih.gov
 Primer A: AACCGAGCCAGACATTC
 Primer B: AGGCTCTCTGTGGCAAGAG
 STS size: 180
 PCR Profile:
 Presoak: 0 degrees C for 0.00 minute(s)
 Denaturation: 92 degrees C for 1.00 minute(s)
 Annealing: 68 degrees C for 2.00 minute(s)
 Polymerization: 72 degrees C for 2.00 minute(s)
 PCR Cycles: 35
 Thermal Cycler: PerkinElmer TC
 Protocol:
 Template: 30-100 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Tag Polymerase: 0.05 units/u1
 Total Vol: 5 u1
 Buffer:
 MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3
 This STS was developed from sequence determined by another
 investigator. See GenBank record: M29423 For additional
 information about the NHGRI chromosome 7 mapping project, see
 http://www.nhgri.nih.gov/DIR/CHR7. Also see Genomics

11:548-64 (1991) [MUID=92128937].
FEATURES
Location/Qualifiers
source
1..976
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="7"
/clone_id="Eric D. Green"
1..976
/gene="PGY1"
253..432
/gene="PGY1"
253..272
/gene="PGY1"
primer_bind
complement(413..432)
ORIGIN
Query Match 100.0%; Score 25; DB 11; Length 976;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGCATCTCCAGAGGACAGATT 25
Db 947 CCAGCATCTCCAGAGGACAGATT 923
RESULT 5
AX597862 1022 bp DNA linear PAT 14-FEB-2003
LOCUS AX597862
DEFINITION Sequence 136 from Patent WO244994.
ACCESSION AX597862
VERSION AX597862.1 GI:28398035
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Brower, M.A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de ardua
Indig, M., Kurensky, D., Luedtke, C., Lukowski, A.A., Lyamichev, V.,
Nett, B.P., Reimer, N.D., Roever, R.T., Skrzypczynski, Z., Ziarno, W.A.,
Comerford, J., Stump, S. and Viegut, D.D.
Systems and method for detection assay production and sale
Patent: WO 0244994-A 136 06-JUN-2002;
JOURNAL THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
Location/Qualifiers
source
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 806 CCAGCATCTCCAGAGGACAGATT 830
RESULT 6
CQ806551 2932 bp DNA linear PAT 10-MAY-2004
LOCUS CQ806551
DEFINITION Sequence 1 from Patent WO2004035803.
ACCESSION CQ806551
VERSION CQ806551.1 GI:47111933
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1

AUTHORS
Roekens, J., Harbeck, N., Koenig, T., Maier, S., Martens, J., Model, F.,
Mimmerich, I., Rujan, T., Schmitt, A., Schmitt, M., Look, M.P. and
Marx, A.
Method and nucleic acids for the improved treatment of breast cell
proliferative disorders
Patent: WO 2004035803-A 1 29-APR-2004;
JOURNAL Epigenomics AG (DE)
FEATURES
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCAGCATCTCCAGAGGACAGATT 25
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RESULT 7
AX457064 2932 bp DNA linear PAT 06-JUL-2002
LOCUS AX457064
DEFINITION Sequence 25 from Patent WO231186.
ACCESSION AX457064
VERSION AX457064.1 GI:21715846
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Berlin, K.
Method for the detection of cytosine methylations
Patent: WO 0231186-A 25 18-APR-2002;
JOURNAL Epigenomics AG (DE)
FEATURES
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RESULT 8
AX598697 2932 bp DNA linear PAT 14-FEB-2003
LOCUS AX598697
DEFINITION Sequence 37 from Patent WO2077272.
ACCESSION AX598697
VERSION AX598697.1 GI:28398833
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J.,
Olek, A., Piepenbrock, C., Adorjan, P., Gröbs, G., Leech, R., Leu, E.,
Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,
Pelet, C. and Ziebarth, H.
Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders

JOURNAL Patent: WO 0207272-2 A 37 03-OCT-2002;
EpiGenomics AG (DE)
FEATURES Location/Qualifiers
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RESULT 9
AX767353/c 2932 bp DNA linear PAT 02-JUL-2003
LOCUS Sequence 1 from Patent WO03044226.
ACCESSION AX767353
VERSION AX767353.1 GI:32435958
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lymphoid cell proliferative disorder
JOURNAL Patent: WO 03044226-A 1 30-MAY-2003;
EpiGenomics AG (DE)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1594 CCAGCATCTCCAGCAGCAGAGTT 1570

RESULT 10
AX795658/c 2932 bp DNA linear PAT 04-OCT-2003
LOCUS Sequence 1 from Patent WO03052135.
ACCESSION AX795658
VERSION AX795658.1 GI:37516324
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S. and Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell proliferative disorder
JOURNAL Patent: WO 03052135-A 1 26-JUN-2003;
EpiGenomics AG (DE)
FEATURES Location/Qualifiers
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ORIGIN /mol_type="unassigned DNA"
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ORIGIN
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DB 1594 CCAGCATCTCCAGCAGCAGAGTT 1570

RESULT 11
AX822109/c 2932 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 1 from Patent EP1340818.
ACCESSION AX822109
VERSION AX822109.1 GI:39748737
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R., Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell proliferative disorder
JOURNAL Patent: EP 1340818-A 1 03-SEP-2003;
EpiGenomics AG (DE)
FEATURES Location/Qualifiers
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DB 1594 CCAGCATCTCCAGCAGCAGAGTT 1570

RESULT 12
AX825749/c 2932 bp DNA linear PAT 11-DEC-2003
LOCUS Sequence 1 from Patent WO03072821.
ACCESSION AX825749
VERSION AX825749.1 GI:39751263
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R., Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell proliferative disorder
JOURNAL Patent: WO 03072821-A 1 04-SEP-2003;
EpiGenomics AG (DE)
FEATURES Location/Qualifiers
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DEFINITION	Human MDRI (multidrug resistance) gene for P-glycoprotein.		
VERSION	X58723 X59732		
KEYWORDS	X58723.1 GI:34532		
SOURCE	MDRI gene; multidrug resistance glycoprotein; P-glycoprotein.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 2932)		
JOURNAL	Kloka, N., Tashbota, J., Kakehi, Y., Komano, T., Gotteaman, M.M.,		
MEDLINE	89322246		
PUBMED	2568832		
REFERENCE	2 (bases 1 to 2932)		
AUTHORS	Kloka, N., Yamano, Y., Komano, T. and Ueda, K.		
TITLE	Heat-shock responsive elements in the induction of the multidrug		
JOURNAL	resistance gene (MDRI)		
MEDLINE	93083619		
PUBMED	1360409		
REFERENCE	3 (bases 1 to 2932)		
AUTHORS	Kloka, N.		
TITLE	Direct Submision		
JOURNAL	Submitted (04-APR-1991) N. Kloka, Laboratory of Biochemistry, Dept		
OF Agricultural Chemistry, Kyoto University, Kitashirakawa			
Olweke-cho, Sakyo-ku Kyoto 606, JAPAN			
See Jpn. J. Cancer Res. 80:1127-1132(1989) for overlapping			
sequence.			
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RESULT 14
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LOCUS
DEFINITION Sequence 683 from Patent WO03013534.
ACCESSION AX706985
VERSION AX706985.1 GI:29563306
KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Heinrich,G. and Kerb,R.
TITLE Methods for the treatment of cancer with irinotecan based on CYP3A5
JOURNAL Patent: WO 03013534-A 683 20-FEB-2003;
Epidaurus Biotechnology AG (DE)
location/Qualifiers
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RESULT 15
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LOCUS
DEFINITION Sequence 683 from Patent WO03013536.
ACCESSION AX707915
VERSION AX707915.1 GI:29563986
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Heinrich,G. and Kerb,R.
TITLE Methods for treatment of cancer using irinotecan based on UGT1A1
JOURNAL Patent: WO 03013536-A 683 20-FEB-2003;
Epidaurus Biotechnology AG (DE)
location/Qualifiers
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 78.592 Seconds
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Title: US-10-007-255-11

Perfect score: 1 ccagcatccacgagcagagtc 25

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	18.8	75.2	601	US-09-949-016-189127	Sequence 189127, A
2	18.8	75.2	601	US-09-949-016-189128	Sequence 189128, A
3	18.6	74.4	2028	US-09-949-016-1153	Sequence 17153, A
4	18.6	74.4	3525	US-09-252-991A-13079	Sequence 13079, A
5	18.6	74.4	3525	US-09-252-991A-12708	Sequence 12708, A
6	18.2	72.8	601	US-09-949-016-164913	Sequence 164913, A
7	18.2	72.8	1894	US-08-615-170-20	Sequence 20, Appl
8	18.2	72.8	1894	US-08-615-170-18	Sequence 18, Appl
9	18.2	72.8	1897	US-08-615-170-18	Sequence 18, Appl
10	18.2	72.8	2087	US-09-949-016-4640	Sequence 4640, Ap
11	18.2	72.8	12588	US-08-387-942C-1	Sequence 16382, A
12	18.2	72.8	36103	US-09-949-016-16382	Sequence 16382, A
13	18.2	72.8	50850	US-09-949-016-15083	Sequence 15083, A
14	18.2	72.8	50850	US-09-949-016-15084	Sequence 15084, A
15	18.2	72.8	50850	US-09-949-016-15085	Sequence 15085, A
16	18.2	72.8	50850	US-09-949-016-21849	Sequence 21849, A
17	18.2	72.0	601	US-09-949-016-83767	Sequence 83767, A
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19	18.2	72.0	5529	US-09-949-016-2415	Sequence 2415, Ap
20	18.2	72.0	6519	US-08-588-985-1	Sequence 1, Appl
21	18.2	72.0	6519	US-08-588-985-1	Sequence 1, Appl
22	18.2	72.0	6519	US-09-949-016-198	Sequence 198, App
23	18.2	72.0	455726	US-09-949-016-14157	Sequence 14157, A
24	18.2	72.0	481115	US-09-949-016-11940	Sequence 11940, A
25	17.8	71.2	601	US-09-949-016-194250	Sequence 194250, A
26	17.8	71.2	5523	US-09-949-016-3952	Sequence 3952, Ap
27	17.8	71.2	22156	US-09-902-540-1195	Sequence 1195, Ap

28	17.8	71.2	312474	US-09-949-016-17434	Sequence 17434, A
29	17.6	70.4	134434	US-09-949-016-17362	Sequence 17362, A
30	17.4	69.6	1671	US-09-902-540-5803	Sequence 5803, Ap
31	17.4	69.6	72704	US-09-902-540-1273	Sequence 1273, Ap
32	17.2	68.8	2181	US-09-949-039A-294	Sequence 294, Appl
33	17.2	68.8	7898	US-08-984-709A-49	Sequence 49, Appl
34	17	68.0	414	US-09-489-039A-295	Sequence 295, App
35	17	68.0	467	US-09-621-976-2241	Sequence 2241, Ap
36	17	68.0	771	US-09-489-039A-419	Sequence 419, Ap
37	17	68.0	972	US-09-902-540-3354	Sequence 3354, Ap
38	17	68.0	1332	US-09-489-039A-220	Sequence 290, App
39	17	68.0	4079	US-09-016-434-1477	Sequence 1477, Ap
40	17	68.0	4353	US-08-365-486A-18	Sequence 18, Appl
41	17	68.0	4353	US-08-880-342-18	Sequence 18, Appl
42	17	68.0	4378	US-09-949-016-1116	Sequence 1116, Ap
43	17	68.0	4382	US-09-949-016-3596	Sequence 3596, Ap
44	17	68.0	4780	US-08-365-486A-20	Sequence 20, Appl
45	17	68.0	4780	US-09-123-708-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
US-09-949-016-189127
Sequence 189127, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949, 016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 189127
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-189127
Query Match 75.2% Score 18.8; DB 4; Length 601;
Best local Similarity 90.9%; Pred. 66;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 221 CCAGCTCCACGAGGCGAGGTT 242
OY 4 GCATCTCCACGAGGCGAGGTT 25
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US-09-949-016-189128
Sequence 189128, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949, 016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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;; SEQ ID NO 189128
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-189128

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Best Local Similarity 90.9%; Pred. No. 66;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATCTCCAGGAGGCGAGATT 25
DB 309 GCAGCTCCAGGAGGCGAGATT 330

RESULT 3
US-09-949-016-17153/c
; Sequence 17153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17153

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Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GCATCTCCAGGAGGCGAGATT 25
DB 28802 GCAGCTCCAGGAGGCGAGATT 28781

RESULT 4
US-09-252-991A-13079/c
; Sequence 13079, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13079
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13079

Query Match 74.4%; Score 18.6; DB 4; Length 2028;
Best Local Similarity 84.0%; Pred. No. 95;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGCGAGATT 25
DB 1187 CCAGCTTGTCAGCAAGGAAGGAGTT 1163

RESULT 5
US-09-252-991A-12708
; Sequence 12708, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; LENGTH: 3525
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12708

Query Match 74.4%; Score 18.6; DB 4; Length 3525;
Best Local Similarity 84.0%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGCGAGATT 25
DB 1998 CCAGCTTGTCAGCAAGGAAGGAGTT 2022

RESULT 6
US-09-252-991A-13251/c
; Sequence 13251, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13251
; LENGTH: 3906
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13251

Query Match 74.4%; Score 18.6; DB 4; Length 3906;
Best Local Similarity 84.0%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGCGAGATT 25
DB 2218 CCAGCTTGTCAGCAAGGAAGGAGTT 2194

RESULT 7

US-09-949-016-164913
Sequence 164913, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 164913
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-164913

Query Match 72.8%; Score 18.2; DB 4; Length 601;
Best Local Similarity 87.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGGAG 23
Db 16 CCAGCACCCTCCAGAGGAG 38

RESULT 8
US-08-615-170-20/c
Sequence 20, Application US/08615170
Patent No. 5776776
GENERAL INFORMATION:
APPLICANT: ORDAHL, Charles P.
APPLICANT: AZAKIE, Anthony
APPLICANT: MAR, Janet H.
APPLICANT: FARRANCE, Iain K.G.
APPLICANT: HALL, Deborah E.
APPLICANT: STEWART, Alexandre F.R.
TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James W.

REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-053120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-615-170-20

Query Match 72.8%; Score 18.2; DB 1; Length 1894;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGAGGAG 24
Db 1054 CGCACCCTCATGAGGAG 1032

RESULT 9
US-08-615-170-18/c
Sequence 18, Application US/08615170
Patent No. 5776776
GENERAL INFORMATION:
APPLICANT: ORDAHL, Charles P.
APPLICANT: AZAKIE, Anthony
APPLICANT: MAR, Janet H.
APPLICANT: FARRANCE, Iain K.G.
APPLICANT: HALL, Deborah E.
APPLICANT: STEWART, Alexandre F.R.
TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James W.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-053120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1897 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-615-170-18

Query Match 72.8%; Score 18.2; DB 1; Length 1897;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGGAGGAGGAGT 24
DB 1057 CGGCACCTCTCCATGAGGAGGAGT 1035

RESULT 10
US-09-949-016-4640/c
Sequence 4640, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4640
LENGTH: 2087
TYPE: DNA
ORGANISM: Human
US-09-949-016-4640

Query Match 72.8%; Score 18.2; DB 4; Length 2087;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGAGGAG 23
DB 319 CCAGCACCTCCAGGAGGAGGAG 297

RESULT 11
US-08-387-942C-1
Sequence 1, Application US/08387942C
Patent No. 5939289
GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA
APPLICANT: VALIA, SVETIN
APPLICANT: SKJAK-BRAEK, GUDMUND
APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNUONAN C-5-EPIMERASE
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: FALIS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C

FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1809-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Azotobacter vinelandii
STRAIN: E
FEATURE:
NAME/KEY: CDS
LOCATION: 290..1951
FEATURE:
NAME/KEY: CDS
LOCATION: 2227..6438
FEATURE:
NAME/KEY: CDS
LOCATION: 6702..9695
FEATURE:
NAME/KEY: CDS
LOCATION: 9973..12588
US-08-387-942C-1

Query Match 72.8%; Score 18.2; DB 2; Length 12588;
Best Local Similarity 87.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGAGGAG 23
DB 8771 CCAGCACCTCTCCAGGAGGAGG 8793

RESULT 12
US-09-949-016-16382/c
Sequence 16382, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16382
LENGTH: 36103
TYPE: DNA
ORGANISM: Human
US-09-949-016-16382

Query Match 72.8%; Score 18.2; DB 4; Length 36103;
Best Local Similarity 87.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGGAGGAGGAG 23

Db 16613 CCAGACTCTCCAGCAAGAGTGAG 16591

RESULT 13

US-09-949-016-15083
Sequence 15083, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15083
LENGTH: 50850
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(50850)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15083

Query Match 72.8%; Score 18.2; DB 4; Length 50850;
Best Local Similarity 87.0%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGCAAGAGTGAGT 24
Db 512 CAGACTCTCCAGCAAGAGTGAGT 534

RESULT 14

US-09-949-016-15084
Sequence 15084, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15084
LENGTH: 50850
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(50850)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15084

Query Match 72.8%; Score 18.2; DB 4; Length 50850;
Best Local Similarity 87.0%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGCAAGAGTGAGT 24
Db 512 CAGACTCTCCAGCAAGAGTGAGT 534

RESULT 15

US-09-949-016-15085
Sequence 15085, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15085
LENGTH: 50850
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(50850)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15085

Query Match 72.8%; Score 18.2; DB 4; Length 50850;
Best Local Similarity 87.0%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CAGCATCTCCAGCAAGAGTGAGT 24
Db 512 CAGACTCTCCAGCAAGAGTGAGT 534

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds
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Title: US-10-007-255-11
Perfect score: 25
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Database : Published Applications NA:*

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20:	/cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq:*
21:	/cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*
22:	/cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	1021	17	US-10-321-039-24
2	25	100.0	2932	18	US-10-473-126-37
3	19.2	76.8	561	18	US-10-767-701-25185
4	19.2	76.8	619	18	US-10-425-115-59217
5	18.6	74.4	60	10	US-09-908-975-9939
6	18.6	74.4	2797	17	US-10-336-603A-7
7	18.6	74.4	2914	17	US-10-336-603A-9
8	18.6	74.4	2963	17	US-10-444-575-5
9	18.6	74.4	2963	17	US-10-440-464-125
10	18.6	74.4	2968	17	US-10-335-603A-11
11	18.6	74.4	3058	9	US-09-964-824A-234

c 12	18.6	74.4	3058	9	US-09-880-107-1654	Sequence 1654, Ap
c 13	18.6	74.4	3058	17	US-10-336-603A-5	Sequence 5, Appl
c 14	18.6	74.4	684187	18	US-10-367-094-71	Sequence 71, Appl
c 15	18.2	72.8	494	13	US-10-027-632-230104	Sequence 230104,
c 16	18.2	72.8	494	13	US-10-027-632-230104	Sequence 230104,
c 17	18.2	72.8	945	13	US-10-027-632-30739	Sequence 30739, A
c 18	18.2	72.8	945	17	US-10-027-632-30739	Sequence 30739, A
c 19	18.2	72.8	1346	9	US-09-805-020-25	Sequence 25, Appl
c 20	18.2	72.8	1422	18	US-10-437-963-75819	Sequence 75819, A
c 21	18.2	72.8	1643	9	US-09-805-020-26	Sequence 26, Appl
c 22	18.2	72.8	1717	9	US-09-805-020-24	Sequence 24, Appl
c 23	18.2	72.8	2083	17	US-10-159-563-289	Sequence 289, Ap
c 24	18.2	72.8	2196	13	US-10-087-192-1799	Sequence 1799, Ap
c 25	18.2	72.8	2345	15	US-10-101-510-504	Sequence 504, App
c 26	18.2	72.8	2713	9	US-09-805-020-27	Sequence 27, Appl
c 27	18.2	72.8	57013	13	US-10-087-192-1798	Sequence 1798, Ap
c 28	18	72.0	201	18	US-10-719-993-2047	Sequence 2047, Ap
c 29	18	72.0	201	18	US-10-719-993-2047	Sequence 2047, Ap
c 30	18	72.0	201	18	US-10-719-993-2047	Sequence 2047, Ap
c 31	18	72.0	2524	17	US-10-152-319A-2092	Sequence 115, App
c 32	18	72.0	2524	17	US-10-152-319A-2092	Sequence 109, App
c 33	18	72.0	6519	18	US-10-719-993-109	Sequence 108, App
c 34	18	72.0	6638	18	US-10-719-993-108	Sequence 6787, Ap
c 35	18	72.0	493999	18	US-10-062-674-773	Sequence 773, App
c 36	17.8	71.2	358	17	US-10-062-674-773	Sequence 226, App
c 37	17.8	71.2	575	11	US-09-876-143-314	Sequence 314, App
c 38	17.8	71.2	575	11	US-09-876-143-314	Sequence 120970,
c 39	17.8	71.2	1003	13	US-10-027-632-120970	Sequence 120971,
c 40	17.8	71.2	1003	13	US-10-027-632-120970	Sequence 120972,
c 41	17.8	71.2	1003	13	US-10-027-632-120970	Sequence 120970,
c 42	17.8	71.2	1003	17	US-10-027-632-120970	Sequence 120971,
c 43	17.8	71.2	1003	17	US-10-027-632-120970	Sequence 120972,
c 44	17.8	71.2	1003	17	US-10-027-632-120970	Sequence 45219, A
c 45	17.8	71.2	1146	17	US-10-369-493-45219	

ALIGNMENTS

RESULT 1
US-10-321-039-24
Sequence 24, Application US/10321039
Publication No. US20040014067A1
GENERAL INFORMATION:
APPLICANT: Lymanchev, Victor
APPLICANT: Lukowiak, Andrew
APPLICANT: Javits, Nancy
APPLICANT: Kurensky, David
TITLE OF INVENTION: Amplification Methods and Compositions
FILE REFERENCE: FORS-06960
CURRENT APPLICATION NUMBER: US/10/321.039
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 09/998,157
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/360,489
NUMBER OF SEQ ID NOS: 759
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 1021
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (561) (561)
OTHER INFORMATION: n can be t or c.
US-10-321-039-24
Query Match 100.0%, Score 25; DB 17; Length 1021;
Best Local Similarity 100.0%, Pred. No. 0.076;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGCAGGACAGATT 25
DB 805 CCAGCATCTCCAGCAGGACAGATT 829

RESULT 2
US-10-473-126-37/c
Sequence 37, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473.126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 37
LENGTH: 2932
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-473-126-37

Query Match 100.0%; Score 25; DB 18; Length 2932;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGCAGGACAGATT 25
DB 1594 CCAGCATCTCCAGCAGGACAGATT 1570

RESULT 3
US-10-767-701-25185
Sequence 25185, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 25185
LENGTH: 561
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: 30948191
US-10-767-701-25185

Query Match 76.8%; Score 19.2; DB 18; Length 561;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CAGCATCTCCAGCAGGACAGATT 25
DB 382 CAGCATCTCTCCGAGGACAGACTT 405

RESULT 4
US-10-425-115-59217
Sequence 59217, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 59217
LENGTH: 619
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_154001C.1
US-10-425-115-59217

Query Match 76.8%; Score 19.2; DB 18; Length 619;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 CAGCATCTCCAGCAGGACAGATT 25
DB 561 CAGCATCTGACGAGGACAAAGTT 584

RESULT 5
US-09-908-975-9939/c
Sequence 9939, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simcha
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9939
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-9939

Query Match 74.4%; Score 18.6; DB 10; Length 60;
Best Local Similarity 84.0%; Pred. No. 76;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGCAGGACAGATT 25
DB 36 CCAGCAGCTCCAGCAAGGCTGACTT 12

RESULT 6
US-10-336-603A-7/c
Sequence 7, Application US/10336603A
Publication No. US20040072997A1
GENERAL INFORMATION:
APPLICANT: Alsobrook et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-533A
CURRENT APPLICATION NUMBER: US/10/336,603A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26

NUMBER OF SEQ ID NOS: 169
SOFTWARE: Cursaeqlist version 0.1
SEQ ID NO 7
LENGTH: 2797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (130)..(2658)
US-10-336-603A-7

Query Match 74.4%; Score 18.6; DB 17; Length 2797;
Best Local Similarity 84.0%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CCAGCATCTCCAGAGGCGAGATT 25
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 7
US-10-336-603A-9/c
Sequence 9, Application US/10336603A
Publication No. US20040072997A1
GENERAL INFORMATION:
APPLICANT: Alsbrook et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-533A
CURRENT APPLICATION NUMBER: US/10/336,603A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Cursaeqlist version 0.1
SEQ ID NO 9
LENGTH: 2914
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (130)..(2775)
US-10-336-603A-9

Query Match 74.4%; Score 18.6; DB 17; Length 2914;
Best Local Similarity 84.0%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CCAGCATCTCCAGAGGCGAGATT 25
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 8
US-10-444-575-5/c
Sequence 5, Application US/10444575
Publication No. US20030232374A1
GENERAL INFORMATION:
APPLICANT: University of Connecticut Health Center
APPLICANT: Kuchel, George A
APPLICANT: Zhu, Qing
TITLE OF INVENTION: Compositions and Methods Relating to Destruxor Estrogen-Regulated
TITLE OF INVENTION: Protein (DERP)
FILE REFERENCE: UCT-0035
CURRENT APPLICATION NUMBER: US/10/444,575
CURRENT FILING DATE: 2003-05-22
PRIOR APPLICATION NUMBER: US 60/382,830
PRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 2963

TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Tobe, T., Saguuchi, K., Hashimoto, K., Miura, N.H., Tomita, M.,
AUTHORS: Li, F., Wang, Y., Minoshima, S., and Shimizu, N.
TITLE: Mapping of human inter-alpha-trypsin inhibitor family heavy
TITLE: chain-related protein gene (ITIH1) to human chromosome 3p21-p14
JOURNAL: Cytogenet. Cell Genet.
VOLUME: 71
ISSUE: 3
PAGES: 296-298
DATE: 1995
DATABASE ACCESSION NUMBER: NM 002218
DATABASE ENTRY DATE: 2003-04-07
RELEVANT RESIDUES: (1)..(2963)
US-10-444-575-5

Query Match 74.4%; Score 18.6; DB 17; Length 2963;
Best Local Similarity 84.0%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CCAGCATCTCCAGAGGCGAGATT 25
Db 1321 CCAGCTTCTCCAGAGGCGATAGCT 1297

RESULT 9
US-10-440-464-125/c
Sequence 125, Application US/10440464
Publication No. US20040018528A1
GENERAL INFORMATION:
APPLICANT: DEPRIMO, SAMUEL
APPLICANT: O'FARRELL, ANNE-MARIE
APPLICANT: MORIMOTO, AYESA
APPLICANT: SMOLICH, BEVERLY
APPLICANT: MANNING, WILLIAM
APPLICANT: WALTER, SARAH
APPLICANT: CHERRINGTON, JULIE
APPLICANT: SCHILLING, JIM
TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
FILE REFERENCE: 038602/1592
CURRENT APPLICATION NUMBER: US/10/440,464
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: 60/380,872
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: 60/448,874
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 125
LENGTH: 2963
TYPE: DNA
ORGANISM: Homo sapiens
US-10-440-464-125

Query Match 74.4%; Score 18.6; DB 17; Length 2963;
Best Local Similarity 84.0%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 CCAGCATCTCCAGAGGCGAGATT 25
Db 1321 CCAGCTTCTCCAGAGGCGATAGCT 1297

RESULT 10
US-10-336-603A-11/c
Sequence 11, Application US/10336603A
Publication No. US20040072997A1
GENERAL INFORMATION:
APPLICANT: Alsbrook et al.

;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;; FILE REFERENCE: 21402-533A
;; CURRENT APPLICATION NUMBER: US/10/336,603A
;; CURRENT FILING DATE: 2003-01-03
;; PRIOR APPLICATION NUMBER: 09/746,491
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: 10/055,569
;; PRIOR FILING DATE: 2001-10-26
;; NUMBER OF SEQ ID NOS: 169
;; SOFTWARE: CuraseqList version 0.1
;; SEQ ID NO 11
;; LENGTH: 2968
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (130)..(2829)
US-10-336-603A-11

Query Match 74.4%; Score 18.6; DB 17; Length 2968;
Best Local Similarity 84.0%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCGAGATT 25
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 11
US-09-964-824A-234/c
;; Sequence 234, Application US/09964824A
;; Patent No. US20020102531A1
;; GENERAL INFORMATION:
;; APPLICANT: Horrigan, Stephen
;; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature
;; FILE REFERENCE: 689290-73
;; CURRENT APPLICATION NUMBER: US/09/964,824A
;; CURRENT FILING DATE: 2001-09-27
;; PRIOR APPLICATION NUMBER: US/60/236,033
;; PRIOR FILING DATE: 2000-09-28
;; PRIOR APPLICATION NUMBER: US/60/236,032
;; PRIOR FILING DATE: 2000-09-28
;; PRIOR APPLICATION NUMBER: US/60/236,028
;; PRIOR FILING DATE: 2000-09-28
;; NUMBER OF SEQ ID NOS: 583
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 234
;; LENGTH: 3058
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-964-824A-234

Query Match 74.4%; Score 18.6; DB 9; Length 3058;
Best Local Similarity 84.0%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCGAGATT 25
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 12
US-09-880-107-1654/c
;; Sequence 1654, Application US/09880107
;; Patent No. US20020142981A1
;; GENERAL INFORMATION:
;; APPLICANT: Horne, Darci T.
;; APPLICANT: Vockley, Joseph G.
;; APPLICANT: Scherf, Uwe
;; APPLICANT: Gene Logic, Inc.
;; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;; FILE REFERENCE: 44921-5028-WO

;; CURRENT APPLICATION NUMBER: US/09/880,107
;; CURRENT FILING DATE: 2001-06-14
;; PRIOR APPLICATION NUMBER: US 60/211,379
;; PRIOR FILING DATE: 2000-06-14
;; PRIOR APPLICATION NUMBER: US 60/237,054
;; PRIOR FILING DATE: 2000-10-02
;; NUMBER OF SEQ ID NOS: 3950
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1654
;; LENGTH: 3058
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D38535
US-09-880-107-1654

Query Match 74.4%; Score 18.6; DB 9; Length 3058;
Best Local Similarity 84.0%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCGAGATT 25
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 13
US-10-336-603A-5/c
;; Sequence 5, Application US/10336603A
;; Publication No. US20040072997A1
;; GENERAL INFORMATION:
;; APPLICANT: Alsbjork et al.
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;; FILE REFERENCE: 21402-533A
;; CURRENT APPLICATION NUMBER: US/10/336,603A
;; CURRENT FILING DATE: 2003-01-03
;; PRIOR APPLICATION NUMBER: 09/746,491
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: 10/055,569
;; PRIOR FILING DATE: 2001-10-26
;; NUMBER OF SEQ ID NOS: 169
;; SOFTWARE: CuraseqList version 0.1
;; SEQ ID NO 5
;; LENGTH: 3058
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (130)..(2919)
US-10-336-603A-5

Query Match 74.4%; Score 18.6; DB 17; Length 3058;
Best Local Similarity 84.0%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGCGAGATT 25
Db 1417 CCAGCTTCTCCAGAGGCGATAGCT 1393

RESULT 14
US-10-367-094-71
;; Sequence 71, Application US/10367094
;; Publication No. US20040170982A1
;; GENERAL INFORMATION:
;; APPLICANT: David W. Morris
;; APPLICANT: Marc Malandro
;; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
;; FILE REFERENCE: 529452001500
;; CURRENT APPLICATION NUMBER: US/10/367,094
;; CURRENT FILING DATE: 2003-02-14
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 71

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; LENGTH: 684187
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(684187)
; OTHER INFORMATION: n = A,T,C or G
US-10-367-094-71

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Query Match          74.4%; Score 18.6; DB 18; Length 684187;
Best Local Similarity 84.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 CCAGCATCTCCACGAGCAGAGTT 25
Db      253637 CCAGCCTCTGCATGATGACAGAGTT 253661

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```

RESULT 15
US-10-027-632-230104/c
; Sequence 230104, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 230104
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-230104

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Query Match          72.8%; Score 18.2; DB 13; Length 494;
Best Local Similarity 87.0%; Pred. No. 12e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      3 AGCATCTCCACGAGCAGAGTT 25
Db      454 AGCACCTCCACGAGCAGAGTT 432

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Search completed: February 9, 2005, 22:26:38
Job time : 268.667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds
(without alignments)
602.360 Million cell updates/sec

Title: US-10-007-255-11
Perfect score: 1
Sequence: 1 ccagcatctccacgaagcagagc 25

Scoring table: IDENTITY NUC
Gapop 10_0, Gapex 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: Geneseq1980s.*
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- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	6	AAD39000 Human mdr
2	25	100.0	25	6	AAD39010 Human mdr
3	25	100.0	2932	8	ABZ09897 Human 5'
4	25	100.0	2932	10	ADB53945 MDR1 geno
5	25	100.0	2932	10	ADBE84005 5' regula
6	25	100.0	2932	13	ADSE88985 Human ABC
7	25	100.0	8573	6	AB598184 Human mdr
8	25	100.0	10200	6	AD41243 Human MDR
9	25	100.0	177380	8	ACF62751 Cancer ba
10	25	100.0	177380	8	ADB20870 MRP1 base
11	25	100.0	177380	10	ADB87959 Human UGT
12	25	100.0	177380	10	ADB96842 Human MDR
13	25	100.0	177380	10	ADB92133 Human MDR
14	18.6	74.4	60	6	ABN37191 Human SPL
15	18.6	74.4	354	12	AD044565 A1480570e
16	18.6	74.4	807	10	ADC39482 Novel hum
17	18.6	74.4	867	10	AD09661 Novel DNA
18	18.6	74.4	1506	12	ADP28080 Human sec
19	18.6	74.4	1506	12	ADP28075 Human sec
20	18.6	74.4	2028	11	ABD14475 Pseudomon

C	21	18.6	74.4	2797	10	ADD49034	ADD49034 Human NOV
C	22	18.6	74.4	2834	12	ADJ72006	ADJ72006 Human PMM
C	23	18.6	74.4	2905	12	ADJ72005	ADJ72005 Human PMM
C	24	18.6	74.4	2914	10	ADD49036	ADD49036 Human NOV
C	25	18.6	74.4	2960	13	ACN37942	ACN37942 Tumour-as
C	26	18.6	74.4	2963	6	ABL41971	ABL41971 DNA seque
C	27	18.6	74.4	2963	12	ADH17126	ADH17126 Human JTI
C	28	18.6	74.4	2963	12	ADH19055	ADH19055 Human Int
C	29	18.6	74.4	2968	10	ADD49038	ADD49038 Human NOV
C	30	18.6	74.4	3058	6	ABL67200	ABL67200 Thyroid C
C	31	18.6	74.4	3058	6	ABL41972	ABL41972 Nucleotid
C	32	18.6	74.4	3058	6	ABN95156	ABN95156 Gene #165
C	33	18.6	74.4	3058	10	ADD49032	ADD49032 Human NOV
C	34	18.6	74.4	3144	10	ADG75752	ADG75752 Human pro
C	35	18.6	74.4	3489	8	ACC59960	ACC59960 Human PMM
C	36	18.6	74.4	3525	11	ABD14104	ABD14104 Pseudomon
C	37	18.6	74.4	3906	11	ABD14647	ABD14647 Pseudomon
C	38	18.6	74.4	4042	10	AD07449	AD07449 Novel cod
C	39	18.6	74.4	4226	12	AD064433	AD064433 Novel hum
C	40	18.6	74.4	5672	13	ACN42394	ACN42394 Human dia
C	41	18.6	74.4	5756	13	ACN42393	ACN42393 Human dia
C	42	18.6	74.4	5783	13	ACN42392	ACN42392 Human dia
C	43	18.6	74.4	5793	13	ACN42391	ACN42391 Human dia
C	44	18.6	74.4	11000	13	ABD32594_2	Continuation (3 of
C	45	18.2	72.8	444	4	AAI79965	AAI79965 Human pol

ALIGNMENTS

RESULT 1

AAD39000 standard; DNA: 25 BP.

23-SEP-2002 (first entry)

Human mdr1-HRE antisense oligonucleotide #3.

Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythemia; myeloma; angioendothelial myeloid metaplasia; myeloid leukaemia; gene therapy; polycythemia vera; hypoxia responsive element; HRE; antisense; phosphorothioate backbone; ss.

Homo sapiens.
Synthetic.

Key modified_base Location/Qualifiers
FT 1..25
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"

WO200234291-A2.

02-MAY-2002.

25-OCT-2001; 2001WO-US049856.

26-OCT-2000; 2000US-0243542P.

(BGM) BRIGHAM & WOMENS HOSPITAL INC.

Colgan SP;

WPI; 2002-471427/50.

Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
PT binding molecules.
XX
PS Claim 14; Page 43; 92pp; English.
XX
CC The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is an antisense
CC oligo targeted to HRE in the mdrl gene (mdrl-HRE) to inhibit its
CC expression. This oligo is used in the exemplification of the invention
XX
SQ Sequence 25 BP; 7 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCACGAGGAGAGTT 25
DB 1 CCAGCATCTCCACGAGGAGAGTT 25

RESULT 2
AAD39010/C
ID AAD39010 standard; DNA; 25 BP.
XX
AC AAD39010;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human mdrl gene HIF-1 binding site DNA #3.
XX
KW Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;
KW hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;
KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
KW myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;
KW angiotenic myeloid metaplasia; myeloid leukaemia; gene therapy;
KW polycythaemia vera; hypoxia responsive element; HRE; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_binding 11..15
FT /*tag= a
FT /bound_moiety= "HIF-1"
XX
PN WO200234291-A2.
XX
PD 02-MAY-2002.
XX
PF 25-OCT-2001; 2001WO-US049856.
XX
PR 26-OCT-2000; 2000US-0243542P.
XX
PA (BCHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Colgan SP;
XX
DR WPI; 2002-471427/50.
XX
PT Treating a subject (at risk of) having a hematologic malignancy or
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
PT binding molecules.
XX
PS Example 2; Page 12; 92pp; English.
XX
CC The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is human mdrl
CC gene HIF-1 binding site DNA
XX
SQ Sequence 25 BP; 4 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCACGAGGAGAGTT 25
DB 25 CCAGCATCTCCACGAGGAGAGTT 1

RESULT 3
ABZ09897/C
ID ABZ09897 standard; DNA; 2932 BP.
XX
AC ABZ09897;
XX
DT 16-JAN-2003 (first entry)
XX
DE Human 5' and/or regulatory region of MDR1 DNA SEQ ID NO:37.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
PN WO20027272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIC-) EPIDENOMICS AG.
XX
PI Berlin K, Braun A, Dietler J, Guertig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwobe I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 38; SEQ ID NO 37; 117pp; English.
XX
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders

CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. AB209861 to AB211118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients

XX
SQ Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 2932;
Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Gaps 0;
Matches 25; Conservative 0; Indels 0;

OY 1 CCAGCATCTCCACGAGCAGAGTT 25
Db 1594 CCAGCATCTCCACGAGCAGAGTT 1570

RESULT 4
ADBS3945/c
ID ADBS3945 standard; DNA; 2932 BP.

XX AC ADBS3945;

XX DT 04-DEC-2003 (first entry)

XX DE MDR1 genomic DNA region.

XX KM colon cell proliferative disorder; non methylated CpG dinucleotide;
XX cytosine; cancer; adenoma; carcinoma; cytosine methylation state; ds.

XX OS Unidentified.

XX FN WO2003072821-A2.

XX PD 04-SEP-2003.

XX PF 27-FEB-2003; 2003WO-EP002035.

XX PR 27-FEB-2002; 2002EP-00004551.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Adorjan P, Burger M, Maier S, Nimrich I, Becker E, Leesche R;
XX Rujan T, Schmitt A;

XX DR WPI; 2003-731620/69.

XX PT Detecting and differentiating between colon cell proliferative disorders
XX associated with a gene or its regulatory regions comprising contacting a
XX target nucleic acid in a biological sample obtained from the subject with
XX a reagent.

XX PS Claim 46; SEQ ID NO 1; 74bp; English.

XX CC The invention relates to a novel method for detecting and differentiating
XX between colon cell proliferative disorders associated with at least one
XX gene or its regulatory regions. The method comprises contacting a target
XX nucleic acid in a biological sample obtained from the subject with at

CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytosine activity whilst the method may useful
CC for detecting and differentiating between colon adenoma and colon carcinoma.
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the genomic DNA region of
CC the invention. This sequence is not shown within the specification but is
CC taken from Wipoweb.

XX
SQ Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 2932;
Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Gaps 0;
Matches 25; Conservative 0; Indels 0;

OY 1 CCAGCATCTCCACGAGCAGAGTT 25
Db 1594 CCAGCATCTCCACGAGCAGAGTT 1570

RESULT 5

ADBE84005/c
ID ADBE84005 standard; DNA; 2932 BP.

XX AC ADBE84005;

XX DT 29-JAN-2004 (first entry)

XX DE 5' regulatory region of human gene MDR1.

XX KM ds; lymphoid cell proliferative disorder; methylation;
XX methylated CpG dinucleotide; single nucleotide polymorphism; SNP;

XX KM diffuse large B-cell lymphoma; mantle cell lymphoma;
XX chronic lymphocytic leukemia; small lymphocytic lymphoma;

XX KM follicular lymphoma; diagnosis; prognosis.

XX OS Homo sapiens.

XX FN WO2003044226-A2.

XX PD 30-MAY-2003.

XX PF 25-NOV-2002; 2002WO-EP013265.

XX PR 23-NOV-2001; 2001DE-01057491.

XX PR 28-DEC-2001; 2001DE-01064501.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimrich I;
XX WPI; 2003-457621/43.

XX PT Detecting and differentiating between lymphoid cell proliferative
XX disorders comprising contacting a target nucleic acid with at least one
XX reagent that distinguishes between methylated and non-methylated CpG
XX dinucleotides.

XX PS Disclosure; SEQ ID NO 1; 448bp; English.

XX CC The invention relates to a method of detecting and differentiating
XX between lymphoid cell proliferative disorders associated with at least
XX one gene and/or their regulatory regions in a subject by contacting a
XX target nucleic acid in a biological sample obtained from the subject with
XX at least one reagent or series of reagents that distinguish between
XX methylated and non-methylated CpG dinucleotides within the target nucleic
XX acid. The genes and/or their regulatory regions are preferably selected
XX from MDR1, CSNK2B, EGFR4, AR, CDK4, RB2, CDC25A, Grib beta, MYO1, CDH3,
XX MYC1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS,
XX GSTR1, HIC-1, MGMT, MHL1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C,

CC GSK3beta, ESR1, APAF1, BAX, or HOXA5. Oligomers, peptide nucleic
 CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
 CC of the genes are useful for detecting the methylation state of all the
 CC CpG dinucleotides within one or more the sequences, or their complements,
 CC for determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs), and for differentiating at least two of the medical
 CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
 CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
 CC lymphoma. They are also useful for detecting of a predisposition to,
 CC differentiation between subclases, diagnosis, prognosis, treating and/or
 CC monitoring of lymphoid cell proliferative disorder. This sequence
 CC represents the 5' and/or regulatory region from one of the above
 CC mentioned genes.

XX Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 2932;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGGAGGAGTT 25
 |||||
 DB 1594 CCAGCATCTCCAGAGGAGGAGTT 1570

RESULT 6
 ADS88985/c
 ID ADS88985 standard; DNA; 2932 BP.

XX ADS88985;
 XX 18-NOV-2004 (first entry)

XX Human ABCB1 gene SEQ ID NO:1.

XX de; gene; human; cell proliferative disorder; breast; methylation;
 KM cytochrome; gene therapy; single nucleotide polymorphism; SNP.

OS Homo sapiens.

PN WO2004035603-A2.

XX 29-APR-2004.

XX 01-OCT-2003; 2003WO-EP010881.

PR 01-OCT-2002; 2002DE-01045779.

PR 07-JAN-2003; 2003DE-01000696.

PR 17-APR-2003; 2003DE-01017955.

PA (EPIG-) EPIGENOMICS AG.

XX Poekens J, Harbeck N, Koenig T, Maier S, Marens J, Model F;
 PI Nimmrich I, Rujan T, Schmitt A, Schmitt M, Look MP, Marx A;
 DR WPI; 2004-348468/32.

XX Predicting responsiveness of a subject with breast cell proliferative
 PT disorder, useful for treating or differentiating breast cell
 PT proliferative disorders comprises analyzing methylation pattern of a
 PT genomic DNA from the subject.

XX Example 2; SEQ ID NO 1; 104pp; English.

XX The invention relates to a novel method for predicting the responsiveness
 CC of a subject with a cell proliferative disorder of the breast tissues to
 CC a therapy comprising analysing the methylation pattern of a target
 CC nucleic acid by contacting at least one of the target nucleic acids in a
 CC biological sample obtained from the subject prior to or during treatment.
 CC The method of the invention has cytosine activity, and may have a use
 CC in gene therapy. The set of oligonucleotides comprising at least two of
 CC the oligomers are useful for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms (SNPs) within the sequences. The

CC methods, nucleic acid, oligonucleotide, and kit are useful for the
 CC treatment, characterization, classification and/or differentiation, of
 CC breast cell proliferative disorder. The method is also useful for
 CC predicting the responsiveness of a subject with a cell proliferative
 CC disorder of the breast tissues to a therapy. The present sequence is used
 CC in the exemplification of the invention.

XX Sequence 2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 13; Length 2932;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCAGAGGAGGAGTT 25
 |||||
 DB 1594 CCAGCATCTCCAGAGGAGGAGTT 1570

RESULT 7
 ABS98184/c
 ID ABS98184 standard; DNA; 8573 BP.

XX ABS98184;

XX 23-DEC-2002 (first entry)

XX Human multidrug resistance gene promoter B and exons 1-3 sequence.

XX Human; de; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;
 KM cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;
 KM adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR12;
 KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KM epoxide hydrolase 2; BPHX; 5-lipoxygenase activating protein; FLAP;
 KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KM HMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KM NADPH quinone oxidoreductase 2; NQO2; sulfoxyltransferase thermolabile; STM;
 KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; UPA;
 KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KM multidrug resistance associated protein 3; cancer; prostate;
 KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KM altered drug metabolism; cardiovascular function; colorectal tumour;
 KM central nervous system; pulmonary; immunological; SNP;
 KM single nucleotide polymorphism.

OS Homo sapiens.

PN WO200257410-A2.

XX 25-JUL-2002.

XX 28-NOV-2001; 2001WO-US044838.

PR 28-NOV-2000; 2000US-00724389.

PA (DNAS-) DNA SCI LAB INC.

XX Guide M, Hall J;
 PI WPI; 2002-698522/75.

XX Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.

XX Example 22; Page 432-437; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1),

CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), catechin S (CTS), cyclooxgenase 2 (COX), diazepam binding
CC inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
CC transferase (HNMT), kallikrein 2 (KLK2), nicotinamide-N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
CC transferase (UGT2B15), urokinase receptor (uPAR), multidrug resistance
CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
CC The polymorphisms in the human genes cited in the invention are useful as
CC genetic linkage markers for locating and characterizing the genes that
CC are responsible for specific traits within the genome and eventually
CC identifying the genes responsible for a variety of disorder-related
CC traits as a result of their e.g., overexpression, constitutive
CC expression, mutation or underexpression, which may be used in diagnosing
CC and/or treating the disorders. The nucleic acid molecules comprising the
CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502B1, AHR,
CC ANMT, EPHX2, GST12, NNMT, NQO2, NR112, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
CC used to screen for altered cardiovascular function, in COX2 for altered
CC susceptibility to colorectal tumors, in DBI or CHMR1 for altered central
CC nervous system function, in FLAP and HNMT for altered pulmonary,
CC immunological or hematological function, in KLK2 for altered serine
CC protease activity in the prostate, in LTF for altered immunological or
CC hematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a
CC polymorphic DNA sequence of the invention
XX

SO Sequence 8573 BP; 2739 A; 1422 C; 1705 G; 2707 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 8573;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGCAGGACAGATT 25
DB 2539 CCAGCATCTCCAGCAGGACAGATT 2515

RESULT 8

AAD41243/C
ID AAD41243 standard; DNA; 10200 BP.

XX AAD41243;

DT 30-OCT-2002 (first entry)

XX Human MDR1 gene 5' flanking region.

XX Human, transgenic; reporter construct; CYP3A4; cytochrome P450;

KW transcriptional regulatory element; xenobiotic; steroid; MDR1;

KM p-glycoprotein; gene; ds.

XX Homo sapiens.

OS WO200236784-A1.

XX PD 10-MAY-2002.

XX 01-NOV-2001; 2001WO-AU001407.

XX 01-NOV-2000; 2000AU-00001161.

XX 10-MAY-2001; 2001AU-00004901.

XX (UNSY) UNIV SYDNEY.
XX Liddle C, Goodwin BJ, Robertson G;
XX PI

XX MPI; 2002-537301/57.

DR Non-human mammal for determining the effect of a compound on regulation

PT of CYP3A4 gene expression, comprises a reporter construct for producing a

PT reporter linked to a transcriptional regulatory nucleic acid from a human

PT CYP3A4 gene.

PS Claim 11; Page 83-92; 95pp; English.

XX The invention relates to generation of non-human transgenic animals

CC comprising a reporter construct for producing a detectable amount of a

CC reporter molecule operably linked to a transcriptional regulatory nucleic

CC acid molecule from the human CYP3A4 gene. The invention also relates to

CC transgenic animal for analyzing CYP3A4 cytochrome P450 gene regulation.

CC The non-human mammal of the invention is useful for determining whether a

CC compound is capable of effecting the transcription of a human CYP3A4

CC gene. It is also useful for determining the effect of a compound such as

CC a xenobiotic or steroid on the regulation of expression of the CYP3A4

CC gene in a human. The present sequence is 5' flanking region of human (p-

CC glycoprotein) MDR1 gene. This sequence is used as a regulatory element in

CC the invention
XX

SO Sequence 10200 BP; 3296 A; 1785 C; 1985 G; 3134 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 10200;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGCAGGACAGATT 25
DB 9817 CCAGCATCTCCAGCAGGACAGATT 9793

RESULT 9

ACF62751/C

ID ACF62751 standard; DNA; 177380 BP.

XX ACF62751;

DT 08-OCT-2003 (first entry)

XX Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.

XX Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;

KW cytochrome P450; subfamily IIA; nifedipine oxidase; polypeptide 5;

KM cytosolic; gene; ds.

XX Unidentified.

OS WO2003013534-A2.

XX PD 20-FEB-2003.

XX 23-JUL-2002; 2002WO-EP008219.

XX 23-JUL-2001; 2001EP-00117608.

XX 24-MAY-2002; 2002EP-00011710.

XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX Heinrich G, Kerb R;
XX MPI; 2003-268144/26.
XX New use of irinotecan for preparation of compositions for treating cancer
XX in subject having genome with variant allele comprising cytochrome P450,
XX subfamily IIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX Disclosure; SEQ ID NO 683; 86pp; English.
XX The present invention describes the use of irinotecan (I) or its
XX derivative for the preparation of a pharmaceutical composition for
XX CC

CC	treating colorectal cancer; cervical cancer; or malignant glioma in a subject having a genome with a variant allele which comprises a cytochrome p450, subfamily IIIA (unfired) gene.
CC	oxidase), polypeptide 5 (CYP5B) polymorphisms (II). (I) and (II) have cytotoxic activity. The therapeutic applications of (I) are improved,
CC	since it is possible to individually treat a subject with an appropriate dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC	potentially harmful effects are efficiently avoided. Unnecessary and
CC	treatment with substances (nonresponders), as well as the development of drug resistances due to suboptimal drug dosing can be avoided. ACP62200
CC	to AC6F2751 and ABM34912 to ABM35013 represent sequences used in the exemplification of the present invention
CC	
SQ	Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;
Query Match	100.0%; Score 25; DB 8; Length 177380;
Best Local Similarity	100.0%; Pred. No. 0.61;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 CCAGCATCTCCACGAAGCGAGGTT 25 141346 CCAGCATCTCCACGAAGCGAGGTT 141322
Dn	
RESULT 10	
ID	AAB20870/C
XX	AAB20870 standard; DNA; 177380 BP.
AC	AAB20870;
DE	MRP1 based cancer related nucleic acid SEQ ID NO:683.
DT	
XX	20-NOV-2003 (first entry)
XX	
DE	
XX	
KW	irinotecan; colorectal cancer; cervical cancer; gastric cancer; lung cancer; ovarian cancer; pancreatic cancer; malignant glioma; variant allele; multidrug resistance protein 1; MRP1; cytosolic; gene; ds.
XX	
OS	Unidentified.
PN	WO2003013533-A2.
PD	20-FEB-2003.
XX	
PF	23-JUL-2002; 2002MO-EP008200.
PR	23-JUL-2001; 2001EP-00117608. 24-MAY-2002; 2002EP-00011710.
FA	(EPIID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX	
P1	Heinrich G., Kern R;
DR	WIPO; 2003-354397/33.
PT	
FT	Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1 polynucleotide.
PS	Disclosure; SEQ ID NO 683; 100bp; English.
CC	The present invention describes a method for the use of irinotecan (I) or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance protein 1 (MRP1).
CC	polynucleotide (II). (I) has cytostatic activity. (I) or its derivative can be used for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject, where the subject is a human

```

CC      (preferably African or Asian) or a mouse. The present sequence represents
XX      a sequence which is used in the exemplification of the present invention.
XX      SQ
SQ      Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;
XX
XX      Query Match          100.0%; Score 25; DB 8; Length 177380;
XX      Best Local Similarity 100.0%; Pred. No. 0.61;
XX      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY      1 CCAGCATCTCCACGAGGACAGATT 25
DB      141346 CCAGCATCTCCACGAGGACAGATT 141322
XX
XX      RESULT 11
XX      ADB87959/C
XX      ID ADB87959 standard; DNA; 177380 BP.
XX      AC ADB87959;
XX      DT 04-DEC-2003 (first entry)
XX      DE Human UGT1A1 gene sequence SEQ ID NO:683.
XX      KM irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;
XX      KM colorectal cancer; cervical cancer; gastric cancer; lung cancer;
XX      KM ovarian cancer; pancreatic cancer; malignant glioma;
XX      KM uridine diphosphate glycosyltransferase1 member A1; gene; de.
XX      OS Homo sapiens.
XX      PN WO2003013536-A2.
XX      PD 20-FEB-2003.
XX      PE 23-JUN-2002; 2002MO-EP008217.
XX      PR 23-JUN-2001; 2001EP-00117608.
XX      PR 24-MAY-2002; 2002EP-00011710.
XX      PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX      PI Heinrich G, Kerb R;
XX      DR WPI; 2003-289896/28.
XX      PT Use of irinotecan to treat cancer patient by determining if patient has
XX      PT variant alleles of UGT1A1 gene, administering increased/decreased amounts
XX      PT of irinotecan based on increased/decreased levels of UGT1A1 gene product.
XX      PS Disclosure; SEQ ID NO 683; 107bp; English.
XX      CC The invention relates to the novel use of irinotecan to treat a patient
XX      CC suffering from cancer. This involves determining if the patient has one
XX      CC or more variant alleles of the UGT1A1 gene, and if the patient has one or
XX      CC more of such variant alleles, irinotecan is administered in an increased
XX      CC or decreased amount in comparison to the amount that is administered
XX      CC without regard to the patient's alleles in the UGT1A1 gene. The invention
XX      CC has cytostatic activity. A composition of the invention acts as a
XX      CC topoisomerase I inhibitor. The method is useful for treating a patient,
XX      CC an animal e.g. mouse or a human, preferably African or Asian, suffering
XX      CC from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,
XX      CC pancreatic cancer or malignant glioma. The present sequence is udes in
XX      CC the exemplification of the invention.
XX      SQ
SQ      Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;
XX
XX      Query Match          100.0%; Score 25; DB 10; Length 177380;
XX      Best Local Similarity 100.0%; Pred. No. 0.61;
XX      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      1 CCAGCATCTCCACGAGGACAGATT 25

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Db 141346 CCAGCATCTCCAGGAGGAGGATT 141322

RESULT 12

ADB96942/c

ID ADB96942 standard; DNA; 177380 BP.

XX

AC ADB96942;

XX

XX

DT 04-DEC-2003 (first entry)

DE Human MDRI related DNA sequence SEQ ID NO:683.

XX

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;

KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

KM multidrug resistance 1; MDRI; cytosstatic; human; Cyp3A5; MRP1; MDRI;

KM TOP1; ds.

XX

XX Homo sapiens.

OS

PN WO2003013537-A2.

XX

PD 20-FEB-2003.

XX

PF 23-JUL-2002; 2002WO-EP008218.

XX

PR 23-JUL-2001; 2001EP-00117608.

PR 24-MAY-2002; 2002EP-00011710.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

PI Heinrich G, Kerb R;

XX

DR WPI; 2003-268145/26.

XX

PT New use of irinotecan for preparation of pharmaceutical compositions for

PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

XX

PS Disclosure; SEQ ID NO 683; 130bp; English.

XX

CC The invention relates to the novel use of irinotecan or its derivative

CC for the preparation of pharmaceutical compositions for treating

CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or

CC malignant glioma in a subject having a genome with a variant allele which

CC comprises a multidrug resistance 1 (MDRI) polynucleotide. A composition

CC of the invention has cytostatic activity. The invention is useful for the

CC preparation of pharmaceutical compositions for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject (preferably human, more preferably African or Asian)

CC or a mouse. The present sequence is used in the exemplification of the

CC invention.

XX

SEQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;

XX

Query Match 100.0%; Score 25; DB 10; Length 177380;

Best Local Similarity 100.0%; Pred. NO. 0.61;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGGAGGAGGATT 25

Db 141346 CCAGCATCTCCAGGAGGAGGATT 141322

RESULT 13

ADB92133/c

ID ADB92133 standard; DNA; 177380 BP.

XX

AC ADB92133;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human MDRI related DNA sequence SEQ ID NO:683.

XX

KM irinotecan; colorectal cancer; cervical cancer; gastric cancer;

KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

KM multidrug resistance 1; MDRI; cytosstatic; human; UGT1A1; MRP1; TOP1; ds.

XX

OS Homo sapiens.

PN WO2003013535-A2.

XX

PD 20-FEB-2003.

XX

PF 23-JUL-2002; 2002WO-EP008220.

XX

PR 23-JUL-2001; 2001EP-00117608.

PR 24-MAY-2002; 2002EP-00011710.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

PI Heinrich G, Kerb R;

XX

DR WPI; 2003-342400/32.

XX

PT New use of irinotecan for preparation of pharmaceutical compositions for

PT treating cancer in subject having genome with variant allele comprising

PT multidrug resistance 1 polynucleotide.

XX

PS Disclosure; SEQ ID NO 683; 104bp; English.

XX

CC The invention relates to a novel use of irinotecan or its derivative for

CC the preparation of a pharmaceutical composition for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject having a genome with a variant allele which comprises

CC a multidrug resistance 1 (MDRI) polynucleotide. A composition of the

CC invention has cytostatic activity. The present sequence is used in the

CC exemplification of the invention.

XX

SEQ Sequence 177380 BP; 58338 A; 32530 C; 31389 G; 55123 T; 0 U; 0 Other;

XX

Query Match 100.0%; Score 25; DB 10; Length 177380;

Best Local Similarity 100.0%; Pred. NO. 0.61;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGGAGGAGGATT 25

Db 141346 CCAGCATCTCCAGGAGGAGGATT 141322

RESULT 14

ABN37191/c

ID ABN37191 standard; DNA; 60 BP.

XX

AC ABN37191;

XX

DT 15-JUL-2002 (first entry)

XX

DE Human spliced transcript detection oligonucleotide SEQ ID NO:9939.

XX

KM Human; mouse; rat; splice transcript; detection; RNA transcript;

KM splice variant; transcriptome; oligonucleotide library; ss.

XX

OS Homo sapiens.

PN WO200210449-A2.

XX

PD 07-FEB-2002.

XX

PF 20-JUL-2001; 2001WO-1B001903.

XX

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX

PA (COMP-) COMPUGEN INC.

XX

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX WPI; 2002-257383/30.
 DR
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a
 PT genome, useful for detecting tissue-, pathology-, and developmental-
 PT specific genes.
 XX
 PS Example 1; SEQ ID NO 9939; 47bp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
 CC transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises several
 CC oligonucleotides, each capable of hybridizing selectively to a set of
 CC messenger RNAs transcribed from a given transcription unit of the genome,
 CC which encodes one or more messenger RNA splice variants. The
 CC oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterizing the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini-
 CC libraries to detect transcripts of a sub-transcriptome under a particular
 CC biological or pathological state, and so allowing the detection of tissue
 CC - and pathology-specific genes such as those genes only expressed in
 CC specific tissue under a specific pathological condition; to detect
 CC developmental specific genes; and to detect RNA transcripts and splice
 CC variants of a transcriptome of a patient suffering from a particular
 CC disorder. AB272753 to AB29589 represent oligonucleotide sequences from
 CC rats, humans and mice, which are used in the exemplification of the
 CC present invention. N.B. The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 60 BP; 16 A; 15 C; 16 G; 13 T; 0 U; 0 Other;
 QY
 Db 1 CCAGCATCTCCAGCAGCGAGCTT 25
 36 CCAGCACTCCACCAAGGCTGACTT 12
 RESULT 15
 ID ADO44565 standard; DNA, 354 BP.
 XX
 AC ADO44565;
 XX
 DT 29-JUL-2004 (first entry)
 DE AI480570expressed sequence tag (EST) fragment.
 XX
 KM CRH; corticotropin-releasing hormone; antidepressant; tranquilizer;
 KM gene therapy; CNS; expressed sequence tag; EST; ds.
 XX
 OS Mus sp.
 XX
 PN WO2004039837-A2.
 PD 13-MAY-2004.
 PF 23-OCT-2003; 2003WO-EP011792.
 XX
 PR 31-OCT-2002; 2002WO-EP012274.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 PI Peeters PJ, Goehlmann HH, Swagemakers SMA, Kass SU, Steckler THW,
 PI Fierens FLP;

XX
 DR WPI; 2004-376160/35.
 DR GENBANK; A1848545.
 XX
 PT Diagnosing a corticotropin-releasing hormone (CRH)-induced gene
 PT expression profile in an individual comprises determining polypeptides
 PT and polynucleotides that mediate the endocrine response to CRH in the
 PT sample.
 XX
 PS Claim 1; SEQ ID NO 31; 84bp; English.
 XX
 CC The invention relates to diagnosing a corticotropin-releasing hormone
 CC (CRH)-induced gene expression profile in an individual. The method
 CC involves determining the level of gene transcription of a gene comprising
 CC a nucleic acid sequence selected from 28 nucleotide sequences fully
 CC defined in the specification or determining the amount of at least one
 CC protein that modulates CRH signaling in the sample, where the protein
 CC comprises 13 amino acid sequences given in the specification. The methods
 CC and composition are useful for diagnosing, treating and/or preventing CRH
 CC metabolism-related disorders, such as CRH-induced depression or stress.
 CC The polynucleotide is used as a marker of CRH signaling in a cell. These
 CC composition and methods may also be used in identifying compounds that
 CC modulate CRH-induced depression and stress. The present sequence
 CC represents a specific example of a gene fragment that is an important
 CC mediator of CRH-induced changes in the CNS.
 XX
 SQ Sequence 354 BP; 107 A; 71 C; 68 G; 108 T; 0 U; 0 Other;
 QY
 Db 1 CCAGCATCTCCAGCAGCGAGCTT 25
 262 CCAGCACTCCACCAAGGCTGACTT 286

Search completed: February 9, 2005, 16:05:56
 Job time : 247.69 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds
(without alignments)
368.593 Million cell updates/sec

Title: US-10-007-255-11

Perfect score: 25
Sequence: 1 ccagcattccacgaagcagagct 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_scat1:*\n2: gb_scat2:*\n3: gb_hlc:*\n4: gb_scat3:*\n5: gb_scat4:*\n6: gb_scat5:*\n7: gb_scat6:*\n8: gb_gsat1:*\n9: gb_gsat2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20.2	80.8	505	1	AV631826 AV631826
2	20.2	80.8	514	1	AV626483 AV626483
3	20.2	80.8	702	8	BZ536972 CGAHH187C
4	20.2	80.8	724	9	CG206154 PUDB607D
5	20.2	80.8	852	9	CG436506 OGVEI07H
6	20.2	80.8	893	8	BZ785280 PUPXK84TB
7	20.2	80.8	955	9	CG436517 OGVEI07H
8	19.8	79.2	550	4	BM257699 521522 MA
9	19.8	79.2	584	1	AL726135 AL726135
10	19.8	79.2	585	5	BX307891 BX307891
11	19.8	79.2	597	1	AL726201 AL726201
12	19.8	79.2	595	1	AV594929 AV594929
13	19.8	79.2	680	5	BX299583 BX299583
14	19.8	79.2	687	7	CR364140 CR364140
15	19.8	79.2	778	7	CN069432 Salamaunde
16	19.2	76.8	390	6	C82708 C82708
17	19.2	76.8	390	6	C83564 C83564
18	19.2	76.8	451	8	B83634 B83634
19	19.2	76.8	481	8	AZ840094 AZ840094
20	19.2	76.8	561	6	CD211773 HSI_64_A0
21	19.2	76.8	573	7	CK755307 aam01-3ms
22	19.2	76.8	575	7	CO997477 aam01-12m
23	19.2	76.8	619	9	FR000396 Z87779 F. rubripes
24	19.2	76.8	627	6	BY722128 BY722128

25	19.2	76.8	652	8	AZ429284 AZ429284
26	19.2	76.8	655	8	AZ362097 1M0107M03
27	19.2	76.8	677	6	CD916489 G608.102A
28	19.2	76.8	748	9	CC576251 CH240.454
29	19.2	76.8	1202	3	AK020597 M8B_m8cu
30	18.8	75.2	244	4	BI403715 M1-P-CP1-
31	18.8	75.2	459	2	BF740661 QV1-HB003-
32	18.8	75.2	580	6	CA501097 WBE4029 C
33	18.8	75.2	591	8	AZ371777 1M0123B19
34	18.8	75.2	595	7	CF180183 CP180183
35	18.8	75.2	851	8	BH516844 B06G507R
36	18.8	75.2	909	4	BI772691 BI772691
37	18.6	74.4	171	8	AQ012740 CIT-HSP-2
38	18.6	74.4	226	2	BE717844 RC4-HT078
39	18.6	74.4	232	2	BF932509 IL2-NT019
40	18.6	74.4	245	2	BE827704 RC2-ET001
41	18.6	74.4	281	1	AV102388 AV102388
42	18.6	74.4	289	1	AA990519 ua63h01.8
43	18.6	74.4	313	2	BE837783 RC2-FN009
44	18.6	74.4	320	2	BE717759 RC4-HT078
45	18.6	74.4	321	4	BG074771 H3139A09-

ALIGNMENTS

RESULT 1
AV631826 505 bp mRNA linear EST 15-DEC-2000
DEFINITION AV631826 Chlamydomonas reinhardtii 5' to 0.04% CO2 Chlamydomonas
reinhartdii cDNA clone LC100d12_r 5', mRNA sequence.

AV631826 GI:10794460
EST.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Bukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 505)
Asamizu,E., Mura,K., Kuchio,K., Inoue,Y., Fukuzawa,H., Ohnaka,K.,

Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2

adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)

JOURNAL MEDLINE PUBMED
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

source
1..505
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="C9"
/db_xref="taxon:3055"
/clone_id="LC100d12_r"
/clone_idb="Chlamydomonas reinhardtii 5' to 0.04% CO2"
/note="Vector: pluescriptII SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"

ORIGIN

Query Match 80.8%; Score 20.2; DB 1; Length 505;
Best local Similarity 88.0%; Pred. No. 4.1e+02;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CCAGCATCTCCACGAAGCAGAGTT 25
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474 CCAGCATCTTCAAAATGACAGATT 498

RESULT 2
AV626483
LOCUS
DEFINITION
AV626483 Chlamydomonas reinhardtii 5' to 0.04% CO2 Chlamydomonas
reinhardtii cDNA clone LCL009h12_r 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
SOURCE

AV626483 514 bp mRNA linear EST 15-DEC-2000
AV626483 Chlamydomonas reinhardtii 5' to 0.04% CO2 Chlamydomonas
reinhardtii cDNA clone LCL009h12_r 5', mRNA sequence.
AV626483 GI:10788763
EST.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 514)
Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohya, K.,
Nakamura, Y., and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
20539644
11089912
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..514
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/mol_type="mRNA"
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/db_xref="taxon:3055"
/clone="LCL009h12_r"
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"

ORIGIN
Query Match 80.8%; Score 20.2; DB 1; Length 514;
Best Local Similarity 88.0%; Pred. No. 4.1e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCACGAGGCGAGATT 25
|||||
Db 463 CCAGCATCTTCACAAATGCGAGATT 487
|||||

RESULT 3
BZ536972
LOCUS
DEFINITION
BZ536972 702 bp DNA linear GSS 16-DEC-2002
OGAH187C ZM2.0.7.1.5 KB Zea mays genomic clone ZMMBMA061C12,
genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

BZ536972 702 bp DNA linear GSS 16-DEC-2002
OGAH187C ZM2.0.7.1.5 KB Zea mays genomic clone ZMMBMA061C12,
genomic survey sequence.
BZ536972
BZ536972.1 GI:27085170
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 702)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Buddiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..702
/organism="Zea mays"
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/strain="B73"
/db_xref="taxon:4577"
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
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ORIGIN
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Best Local Similarity 88.0%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGCATCTCCACGAGGCGAGATT 25
|||||
Db 367 CCAGCATCTGCACGAGGCGAAAGTT 343
|||||

RESULT 4
CG206154/c
LOCUS
DEFINITION
CG206154/c 724 bp DNA linear GSS 21-AUG-2003
PUDB60TD ZM.0.6.1.0 KB Zea mays genomic clone ZMMBTA0640J24,
genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

CG206154 724 bp DNA linear GSS 21-AUG-2003
PUDB60TD ZM.0.6.1.0 KB Zea mays genomic clone ZMMBTA0640J24,
genomic survey sequence.
CG206154
CG206154.1 GI:34097215
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 724)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSes: PUDB60TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..724
/organism="Zea mays"
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COT selected genomic DNA library"

RESULT 5
CG436506
LOCUS
DEFINITION OGVGE10TH ZM 0.7.1.5_KB Zea mays genomic clone ZMMBma0475A19,
 genomic survey sequence.
ACCESSION CG436506
VERSION CG436506.1 GI:34813045
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 852)
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: OGVGE10TV
 Contact: Cathy Whitelaw
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: sheared ends.
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 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CCAGCATCTCCAGAGGCAAGATT 25
 Db 818 CCAGCATCTGCACGAGGCAAGATT 842
RESULT 6
BZ785280/c
LOCUS PUPAX84TB ZM 0.6.1.0_KB Zea mays genomic clone ZMMBTa277N24,
 genomic survey sequence.
ACCESSION BZ785280
VERSION BZ785280.1 GI:28978677
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SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 893)
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Contact: Cathy Whitelaw
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: sheared ends.
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 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CCAGCATCTCCAGAGGCAAGATT 25
 Db 415 CCAGCATCTGCACGAGGCAAGATT 391
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CG436517/c
LOCUS OGVGE10TV ZM 0.7.1.5_KB Zea mays genomic clone ZMMBma0475A19,
 genomic survey sequence.
ACCESSION CG436517
VERSION CG436517.1 GI:34813056
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 955)
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: OGVGE10TH
 Contact: Cathy Whitelaw
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TP
 Class: sheared ends.
FEATURES Location/Qualifiers
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 methylation filtered genomic DNA library"
ORIGIN
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 Best Local Similarity 88.0%; Pred. No. 4.5e+02;
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 QY 1 CCAGCATCTCCAGAGGCAAGATT 25
 Db 310 CCAGCATCTGCACGAGGCAAGATT 286

RESULT 8
BM257699/c 550 bp mRNA linear EST 17-DEC-2001

LOCUS BM257699
DEFINITION 521522 MARC 3BOV Bos taurus CDNA 5', mRNA sequence.
ACCESSION BM257699
VERSION BM257699.1 GI:17893298
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 550)
Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Caeas, E., Wray, J.E., White, J., Cho, J., Fairbank, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perera, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

TITLE JOURNAL MEDLINE PUBMED
21180013
11282978

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smtlth@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -mnscore 18 and -mismatch 12 options.
PCR primers
FORWARD: AGGAGACGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 125 row: D column: 5
Seq primer: ATTAGCTGACACTATAG.
Location/Qualifiers
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/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

ORIGIN

Query Match 79.2%; Score 19.8; DB 4; Length 550;
Best Local Similarity 91.3%; Pred. No. 6.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGGAGGAG 23
122 CCAGCAGCTCCAGGAGCTGAG 100

Db

RESULT 9
AL726135 584 bp mRNA linear EST 18-APR-2002

LOCUS AL726135
DEFINITION AL726135 Dario rerio embryonic inner ear substracted CDNA Dario
ACCESSION AL726135
VERSION AL726135.1 GI:20190739
KEYWORDS EST.
SOURCE Dario rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Dario.
1 (bases 1 to 584)
Coimbra, R., Weil, D., Brothier, P., Blanchard, S., Levi, M., Harelid, J.P., Weissenbach, J. and Petit, C.
A substracted CDNA library from the zebrafish (Dario rerio) embryonic inner ear
Unpublished (2002)
JOURNAL
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1..584
/organism="Dario rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0A083ZH02"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Dario rerio embryonic inner ear substracted CDNA"
/note="substracted CDNA library"

ORIGIN

Query Match 79.2%; Score 19.8; DB 1; Length 584;
Best Local Similarity 91.3%; Pred. No. 6.3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGCATCTCCAGGAGGAGATT 25
299 AGCATCTCCAGGAGGAGATT 321

Db

RESULT 10
BX307891 585 bp mRNA linear EST 11-MAY-2004

LOCUS BX307891 tcaay Oncorhynchus mykiss CDNA clone tcaay0016b.m.17 5prim,
DEFINITION mRNA sequence.
ACCESSION BX307891
VERSION BX307891.2 GI:42616971
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 585)
Govoroun, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized CDNA libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
JOURNAL
COMMENT On Apr 7, 2003 this sequence version replaced gi:29588536.
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenauporte@jouy.inra.fr to obtain the chromatogram of this sequence.
Plate: 0016 row: m column: 17
Seq primer: M13R.
Location/Qualifiers
1..585
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcaay0016b.m.17"
/tissue_type="adipose tissue, blood, brain, differentiating gonads, gills, interrenal, intestine, kidney, liver, muscle, ovary, pituitary, testis"

/dev_stage="from embryos to adults"
 /lab_host="DH10B"
 /clone_lib="lccay"
 /note="Vector: pT713D-Pac; Rainbow trout multi-tissues -
 normalized + 1 subtraction (lccay) ; Clone distribution :
 AGNNAE Resource centre, Francois PIML,
 Francois.Piml@jouy.inra.fr, INRA, CEA Radiobiologie et
 Etude du genome (LREG), Domaine de Vilvert, 78352,
 Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
 (0) 1.34.65.22.73"

ORIGIN

Query Match 79.2%; Score 19.8; DB 5; Length 585;
 Best Local Similarity 91.3%; Pred. No. 6.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAGCATCTCCAGAGGACAGGT 24
 |||||
 Db 82 CACCATCTCCAGAGGACAGGT 60

RESULT 11
 AL726201/c 587 bp mRNA linear EST 18-APR-2002

LOCUS AL726201 Danio rerio embryonic inner ear subtracted cDNA Danio
 DEFINITION rerio cDNA clone BNOA0832H02 3', mRNA sequence.

ACCESSION AL726201 GI:20190805

VERSION EST

KEYWORDS

SOURCE

ORGANISM

Danio rerio (zebrafish)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE.
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

source

1..587

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="BNOA0832H02"

/tissue_type="inner ear"

/dev_stage="embryonic"

/clone_lib="Danio rerio embryonic inner ear subtracted
 cDNA"

/note="subtracted cDNA library"

ORIGIN

Query Match 79.2%; Score 19.8; DB 1; Length 587;
 Best Local Similarity 91.3%; Pred. No. 6.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGCATCTCCAGAGGACAGATT 25
 |||||
 Db 289 AGCATCTCCAGAGGACAGATT 267

RESULT 12

AV594929/c 595 bp mRNA linear EST 27-NOV-2001

LOCUS AV594929 Bos taurus cartilage fetus Bos taurus cDNA clone

DEFINITION E1C0016F04 5', mRNA sequence.

ACCESSION AV594929

VERSION AV594929.1 GI:9711387

KEYWORDS
 SOURCE
 ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

11713328

Contact: Yoshikazu Sugimoto

Animal Genetics Division

Shirakawa Institute of Animal Genetics

Oakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641

Fax: 81-248-25-5725

Email: kazunugi@cocoa.ocn.ne.jp

Single pass sequencing.

This clone was obtained from a polyA-deleted cDNA library.

Location/Qualifiers

1..595

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/clone="E1C0016F04"

/tissue_type="cartilage"

/dev_stage="fetus"

/lab_host="DH10B"

/clone_lib="Bos taurus cartilage fetus"

/note="Vector: pZL1; Site_1: SalI; Site_2: NotI; Poly A
 was deleted from a NotI site"

ORIGIN

Query Match 79.2%; Score 19.8; DB 1; Length 595;
 Best Local Similarity 91.3%; Pred. No. 6.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAGCATCTCCAGAGGACAG 23
 |||||
 Db 223 CCAGCATCTCCAGAGGACAG 201

RESULT 13

BX299583/c 680 bp mRNA linear EST 10-MAY-2004

LOCUS BX299583 tccay Oncorhynchus mykiss cDNA clone tccay0004b.1.10 5prim,

DEFINITION mRNA sequence.

ACCESSION BX299583

VERSION BX299583.2 GI:42613178

KEYWORDS

SOURCE

ORGANISM

Oncorhynchus mykiss (rainbow trout)

Oncorhynchus mykiss

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 680)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Apr 7, 2003 this sequence version replaced gi:29580228.
 Contact: Guiguen Y
 INRA - SCRIBR
 Campus de Beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us

at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.

Plate: 0004 row: 1 column: 10
Seq primer: M13R.

FEATURES

Location/Qualifiers

1..680
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcay0004b.i.10"
/tissue_type="adipose tissue, blood, brain, differentiating gonads, gills, interrenal, intestine, kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tcay"
/note="Vector: pT7T3D-pac; Rainbow trout multi-tissues - normalized + 1 subtraction (tcay) ; Clone distribution : AGENAE Resource centre. Francois Piumi, Francois Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LRBG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

ORIGIN

Query Match 79.2%; Score 19.8; DB 5; Length 680;
Best Local Similarity 91.3%; Pred. No. 6.4e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGCATCTCCAGAGGACAGT 24

Db 293 CACCATCTCCAGAGGACAGT 271

RESULT 14 CR364140 687 bp mRNA linear EST 21-APR-2004
LOCUS CR364140 AGENAE Rainbow trout normalized testis library (tcbl)
DEFINITION Oncorhynchus mykiss cDNA clone tcbl0038c.j.24 5prim, mRNA sequence.
VERSION CR364140
ACCESSION CR364140.1 GI:46475452
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE 1 (bases 1 to 687)
Govoroun, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cDNA libraries in rainbow trout, *Oncorhynchus mykiss*
Unpublished (2003)
CONTACT: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.
Plate: 0038, row: 1 column: 24.
Seq primer: M13R.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2003)

CONTACT: Guiguen Y

INRA - SCRIBE

Campus de Beaulieu, RENNES cedex, 35042, France

Tel: 02.23.48.50.09

Fax: 02.23.48.50.20

Email: Yann.Guiguen@beaulieu.rennes.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.

Plate: 0038, row: 1 column: 24.

Seq primer: M13R.

FEATURES

Location/Qualifiers

1..687
/organism="Oncorhynchus mykiss"
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/clone_lib="AGENAE Rainbow trout normalized testis library (tcbl)"

ORIGIN

Query Match 79.2%; Score 19.8; DB 7; Length 687;
Best Local Similarity 91.3%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGCATCTCCAGAGGACAGT 24

Db 153 CACCATCTCCAGAGGACAGT 131

RESULT 15 CN069432 778 bp mRNA linear EST 30-MAR-2004
LOCUS CN069432/c Salamander_28_M15.ab1 AG Ambystoma tigrinum tigrinum cDNA, mRNA
DEFINITION sequence.
ACCESSION CN069432
VERSION CN069432.1 GI:45833842
KEYWORDS EST.
SOURCE Ambystoma tigrinum tigrinum (Eastern tiger salamander)
ORGANISM Ambystoma tigrinum tigrinum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandridae; Ambystomatidae; Ambystoma.

REFERENCE 1 (bases 1 to 778)
Putra, S., Smith, J.J., Walker, J.A., Rondet, M., Weisrock, D., Monaghan, J., Samuels, A.K., Kump, K., King, D.C., Maness, N.J., Habermann, B., Tanaka, E., Bryant, S.V., Gardiner, D.M., Patchy, D.M. and Voss, S.R.
From biomedicine to natural history research: EST resources for ambystomatid salamanders
BMC Genomics 5 (1), 54 (2004)
CONTACT: SR Voss
Department of Biology
University of Kentucky
TH Morgan Building, Lexington, KY 40506, USA
Tel: 859 257 9888
Fax: 859 257 1717
Email: svoss@uky.edu
The EST is quality trimmed at the ends with a 20 base window and quality threshold of 15 (phred quality score). Please visit <http://salamander.uky.edu> for any information (trace, quality files etc) regarding this EST.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2004)

CONTACT: SR Voss

Department of Biology

University of Kentucky

TH Morgan Building, Lexington, KY 40506, USA

Tel: 859 257 9888

Fax: 859 257 1717

Email: svoss@uky.edu

The EST is quality trimmed at the ends with a 20 base window and quality threshold of 15 (phred quality score). Please visit <http://salamander.uky.edu> for any information (trace, quality files etc) regarding this EST.

FEATURES

source

Location/Qualifiers

1..778

/organism="Ambystoma tigrinum tigrinum"

/mol_type="mRNA"

/sub_species="tigrinum"

/db_xref="taxon:43116"

/tissue_type="liver, lung, kidney, heart, gonad, brain and gill tissues collected from metamorphosing larvae"

/clone_lib="AG"

ORIGIN

Query Match 79.2%; Score 19.8; DB 7; Length 778;
Best Local Similarity 91.3%; Pred. No. 6.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGCATCTCCAGAGGACAG 23

Db 646 CCAGCATCTCCAGAGGACAG 624

Search completed: February 9, 2005, 21:55:37
Job time : 2451.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds
(without alignments)
2517.530 Million cell updates/sec

Title: US-10-007-255-12

Perfect score: 1 agcttcacacacgctgaatccta 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_gts:*
12: gb_by:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX504309 Sequence
2	25	100.0	25	6	AX504326 Sequence
3	25	100.0	120	6	BD160755 Sequence
4	25	100.0	120	6	BD160756 Kit for a
5	25	100.0	172	6	CQ110210 Sequence
6	25	100.0	172	6	CQ148922 Sequence
7	25	100.0	172	6	CQ232195 Sequence
8	25	100.0	172	6	CQ307508 Sequence
9	25	100.0	172	6	CQ344374 Sequence
10	25	100.0	201	11	BV202141 Sequence
11	25	100.0	201	11	BV202142 Sequence
12	25	100.0	209	9	HUMGP1B002
13	25	100.0	219	6	CQ149621 Sequence
14	25	100.0	219	6	CQ308221 Sequence
15	25	100.0	219	6	CQ345026 Sequence
16	25	100.0	463	6	CQ097020 Sequence
17	25	100.0	463	6	CQ135831 Sequence
18	25	100.0	463	6	CQ219128 Sequence
19	25	100.0	463	6	CQ294934 Sequence

20	25	100.0	463	6	CQ31579 Sequence
21	25	100.0	473	6	CQ136561 Sequence
22	25	100.0	473	6	CQ295678 Sequence
23	25	100.0	473	6	CQ312256 Sequence
24	25	100.0	807	6	I08556 Sequence 1
25	25	100.0	807	6	AR363343 Sequence
26	25	100.0	966	9	HUMMDR1A07
27	25	100.0	3840	6	AX481416 Sequence
28	25	100.0	3843	6	BD171402 Method fo
29	25	100.0	3852	9	AF537133 Macaca mu
30	25	100.0	3852	9	AF537134 Macaca fa
31	25	100.0	3852	9	AF582534 Macaca mu
32	25	100.0	3860	6	AX322787 Sequence
33	25	100.0	3860	6	AX322789 Sequence
34	25	100.0	3988	6	BD190394 Phosphati
35	25	100.0	3988	6	AR452556 Sequence
36	25	100.0	3988	6	AR452554 Sequence
37	25	100.0	4186	6	AR399194 Sequence
38	25	100.0	4186	6	AX108654 Sequence
39	25	100.0	4186	6	AF016535 Homo sapi
40	25	100.0	4195	6	AR399195 Sequence
41	25	100.0	4195	6	AX108656 Sequence
42	25	100.0	4264	6	AR051647 Sequence
43	25	100.0	4264	6	AR051650 Sequence
44	25	100.0	4378	6	E02326 Multidrug r
45	25	100.0	4553	6	CQ716151 Sequence

ALIGNMENTS

RESULT 1	AX504309	Sequence 12 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504309					
DEFINITION	AX504309					
ACCESSION	AX504309.1	GI:23386127				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE	1	Colgan,S.P.				
AUTHORS		Compositions and methods for treating hematologic malignancies and				
TITLE		multiple drug resistance				
JOURNAL		Patent: WO 0234291-A 12 02-MAY-2002;				
FEATURES		THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)				
ORIGIN		location/Qualifiers				
		1..25				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match	100.0%	Score 25;	DB 6;	Length 25;		
Best Local Similarity	100.0%	Pred. No. 0.059;				
Matches	25;	Conservative	0;	Mismatches	0;	Indels
Q1	1	AGCTTCACACACGCTGAATCCTA	25			
DB	1	AGCTTCACACACGCTGAATCCTA	25			
RESULT 2	AX504326/c	Sequence 29 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504326					
DEFINITION	AX504326					
ACCESSION	AX504326.1	GI:23386138				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					

```

REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE          1
JOURNAL        Colgan, S.P.
                Compositions and methods for creating hematologic malignancies and
                multiple drug resistance
                Patent: WO 0234291-A 29 02-MAY-2002;
                THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
FEATURES
SOURCE          Location/Qualifiers
                1..25
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
ORIGIN
Query Match    100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACGCTGTAATCCTA 25
Db 25 AGCTTCCACCAACGCTGTAATCCTA 1

RESULT 3
LOCUS          BD160755 120 bp DNA linear PAT 17-JAN-2003
DEFINITION    Kit for assaying MDRI gene expression level.
ACCESSION     BD160755
VERSION       BD160755.1 GI:27866513
KEYWORDS      JP 2002153274-A/3.
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 120)
AUTHORS       Ujile,T., Hayashi,T., Kawase,M. and Ueji,F.
TITLE         Kit for assaying MDRI gene expression level
JOURNAL       Patent: JP 2002153274-A 3 28-MAY-2002;
              KAINOS LAB INC
COMMENT       OS Artificial Sequence
              PN JP 2002153274-A/3
              PD 28-MAY-2002 JP 2000351224
              PF 17-NOV-2000 JP 2000351224
              PI TAKESHI UJILE,TSUKASA HAYASHI,MASAKO KAWASE,FUMIYAKI UEJI PC
              CC C12N15/09,C12Q1/68,C12N15/00
              CC Kit for assaying MDRI gene expression level
              FH Key Location/Qualifiers
              FT source 1..120
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              Location/Qualifiers
                1..120
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                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
ORIGIN
Query Match    100.0%; Score 25; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACGCTGTAATCCTA 25
Db 79 AGCTTCCACCAACGCTGTAATCCTA 55

RESULT 4
LOCUS          BD160756 120 bp DNA linear PAT 17-JAN-2003
DEFINITION    Kit for assaying MDRI gene expression level.
ACCESSION     BD160756
VERSION       BD160756.1 GI:27866514
KEYWORDS      JP 2002153274-A/4.
SOURCE        synthetic construct

```

```

ORGANISM      synthetic construct
other sequences; artificial sequences.
REFERENCE     1 (bases 1 to 120)
AUTHORS       Ujile,T., Hayashi,T., Kawase,M. and Ueji,F.
TITLE         Kit for assaying MDRI gene expression level
JOURNAL       Patent: JP 2002153274-A 4 28-MAY-2002;
              KAINOS LAB INC
COMMENT       OS Artificial Sequence
              PN JP 2002153274-A/4
              PD 28-MAY-2002 JP 2000351224
              PF 17-NOV-2000 JP 2000351224
              PI TAKESHI UJILE,TSUKASA HAYASHI,MASAKO KAWASE,FUMIYAKI UEJI PC
              CC C12N15/09,C12Q1/68,C12N15/00
              CC Kit for assaying MDRI gene expression level
              FH Key Location/Qualifiers
              FT source 1..120
              /organism='Artificial Sequence'.
              Location/Qualifiers
                1..120
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
ORIGIN
Query Match    100.0%; Score 25; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACGCTGTAATCCTA 25
Db 42 AGCTTCCACCAACGCTGTAATCCTA 66

RESULT 5
LOCUS          CQ110210 172 bp DNA linear PAT 21-JAN-2004
DEFINITION    Sequence 19069 from Patent WO0157272.
ACCESSION     CQ110210
VERSION       CQ110210.1 GI:41079573
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
              Human genome-derived single exon nucleic acid probes useful for
              analysis of gene expression in human placenta
              Patent: WO 0157272-A 19069 09-AUG-2001;
              Aeomica, Inc. (US)
FEATURES
SOURCE          Location/Qualifiers
                1..172
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="MAP TO AC005068.1-EXPRESSED IN PLACENTA, SIGNAL =
                0.64-SWISSPROT HIT: P08183, EVALUE 3.00e-27-NT HIT:
                AF016535.1, EVALUE 2.00e-92-EST_HUMAN HIT: AM847648.1,
                EVALUE 2.30e+00"
ORIGIN
Query Match    100.0%; Score 25; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACGCTGTAATCCTA 25
Db 62 AGCTTCCACCAACGCTGTAATCCTA 86

RESULT 6
LOCUS          CQ148922 172 bp DNA linear PAT 21-JAN-2004

```

DEFINITION Sequence 18944 from Patent WO0157276.
ACCESSION CQ148922
VERSION CQ148922.1 GI:41156272
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 18944 09-AUG-2001;
Neomica, Inc. (US)
FEATURES
source 1.172
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC005068.1-EXPRESSED IN BONE MARROW, SIGNAL = 0.53-SWISSPROT HIT: P08183, EVALUE 3.00e-27-NT HIT: AF016535.1, EVALUE 2.00e-92-EST_HUMAN HIT: AW847648.1, EVALUE 2.30e+00"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCACTGTAAATCCTA 25
|||||
62 AGCTTCCACCACTGTAAATCCTA 86

RESULT 7
CQ322195 172 bp DNA linear PAT 21-JAN-2004
DEFINITION Sequence 19034 from Patent WO0157273.
ACCESSION CQ322195
VERSION CQ322195.1 GI:41215413
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> 04 February 2000 (04.02.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000 (03.10.00)<150> US 60/236,359<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 21 September 2000 (21.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine
JOURNAL Patent: WO 0157273-A 19034 09-AUG-2001;
Neomica, Inc. (US)
FEATURES
source 1.172
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC005068.1-EXPRESSED IN ADULT LIVER, SIGNAL = 0.73-NT HIT: AF016535.1, EVALUE 2.00e-92-SWISSPROT HIT: P08183, EVALUE 3.00e-27-EST_HUMAN HIT: AW847648.1, EVALUE 2.30e+00"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCACTGTAAATCCTA 25
|||||
62 AGCTTCCACCACTGTAAATCCTA 86

RESULT 8
CQ307508 172 bp DNA linear PAT 23-JAN-2004
LOCUS CQ307508
DEFINITION Sequence 16613 from Patent WO0186003.
ACCESSION CQ307508
VERSION CQ307508.1 GI:41268085
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human lung
JOURNAL Patent: WO 0186003-A 18613 15-NOV-2001;
Neomica, Inc. (US)
FEATURES
source 1.172
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC005068.1-EXPRESSED IN LUNG, SIGNAL = 0.65-SWISSPROT HIT: P08183, EVALUE 3.00e-27-NT HIT: AF016535.1, EVALUE 2.00e-92-EST_HUMAN HIT: AW847648.1, EVALUE 2.30e+00"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCACTGTAAATCCTA 25
|||||
62 AGCTTCCACCACTGTAAATCCTA 86

RESULT 9
CQ344374 172 bp DNA linear PAT 23-JAN-2004
LOCUS CQ344374
DEFINITION Sequence 18468 from Patent WO0157275.
ACCESSION CQ344374
VERSION CQ344374.1 GI:41293445
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 18468 09-AUG-2001;
Neomica, Inc. (US)
FEATURES
source 1.172
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC005068.1-EXPRESSED IN BRAIN, SIGNAL = 0.64-SWISSPROT HIT: P08183, EVALUE 3.00e-27-NT HIT: AF016535.1, EVALUE 2.00e-92-EST_HUMAN HIT: AW847648.1, EVALUE 2.30e+00"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACCGGTAAATCCTA 25
 |||
 Db 62 AGCTTCCACCAACCGGTAAATCCTA 86

RESULT 10
 BV202141/c
 LOCUS
 DEFINITION sqm208303 Human DNA (Sequencm) Homo sapiens STS genomic, sequence
 tagged site.
 ACCESSION BV202141
 VERSION BV202141.1 GI:48171155
 KEYWORDS STS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 201)
 Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
 Cantor,C.R. and Braun,A.
 Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
 Regions
 Genome Res. (2004) In press

TITLE
 JOURNAL
 COMMENT
 Contact: Andreas Braun
 Pharmaceuticals division
 Sequenom, Inc.
 3595 John Hopkins Court, San Diego, CA 92121, USA
 Tel: 18582029018
 Fax: 18582029020
 Email: abraun@sequenom.com
 Primer A: No primer sequence submitted
 Primer B: No primer sequence submitted
 STS size: 201.

FEATURES
 source
 1..201
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Human DNA (Sequencm)"
 <1..>201

ORIGIN
 STS
 Query Match 100.0%; Score 25; DB 11; Length 201;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACCGGTAAATCCTA 25
 |||
 Db 188 AGCTTCCACCAACCGGTAAATCCTA 164

RESULT 11
 BV202142/c
 LOCUS
 DEFINITION sqm208304 Human DNA (Sequencm) Homo sapiens STS genomic, sequence
 tagged site.
 ACCESSION BV202142
 VERSION BV202142.1 GI:48171156
 KEYWORDS STS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 201)
 Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
 Cantor,C.R. and Braun,A.
 Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
 Regions
 Genome Res. (2004) In press

TITLE
 JOURNAL
 COMMENT
 Contact: Andreas Braun

Pharmaceuticals division
 Sequenom, Inc.
 3595 John Hopkins Court, San Diego, CA 92121, USA
 Tel: 18582029018
 Fax: 18582029020
 Email: abraun@sequenom.com
 Primer A: No primer sequence submitted
 Primer B: No primer sequence submitted
 STS size: 201.

FEATURES
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Human DNA (Sequencm)"
 <1..>201

ORIGIN
 STS
 Query Match 100.0%; Score 25; DB 11; Length 201;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACCGGTAAATCCTA 25
 |||
 Db 187 AGCTTCCACCAACCGGTAAATCCTA 163

RESULT 12
 HUMGPLEU02/c
 LOCUS HUMGPLEU02 209 bp DNA linear PRI 13-FEB-1996
 DEFINITION Human MDR1/P-glycoprotein gene, exon 7.
 ACCESSION M37724
 VERSION M37724.1 GI:183537
 KEYWORDS glycoprotein.
 SEGMENT 2 of 3
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 209)
 Gekeler,V., Weger,S. and Probst,H.
 mdrl/P-glycoprotein gene segments analyzed from various human
 leukemic cell lines exhibiting different multidrug resistance
 profiles

TITLE
 JOURNAL Biochem. Biophys. Res. Commun. 169 (2), 796-802 (1990)
 MEDLINE 9020529
 PUBMED 1972623
 COMMENT Original
 FEATURES
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 1..209
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="7q21"
 /cell_line="CCRF-CEM"
 /cell_type="T-lymphoblast"
 <1..53
 /gene="PGY1"
 /note="glycoprotein intron 6"
 complement(1..19)
 <94..>209
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 /product="glycoprotein"
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 /db_xref="GDB:G00-120-712"
 /translation="DVSKINEGIDKIGMFQSWATFTGPIVGTGKWLKLT"
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 /note="G00-120-712"
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 intron
 CDS
 primer_bind
 primer_bind

ORIGIN /gene="PGY1"

Query Match 100.0%; Score 25; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAAACCGTGAATCCTA 25
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DB 204 AGCTTCCAAACCGTGAATCCTA 180

RESULT 13
CQ345026/c
LOCUS Sequence 19120 from Patent WO0157275.
DEFINITION CQ345026
ACCESSION CQ345026.1 GI:41294097
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157275-A 19120 09-AUG-2001;
Aeomica, Inc. (US)

FEATURES
source location/Qualifiers
1..219
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="MAP TO AC002457.1-EXPRESSED IN BONE MARROW, SIGNAL = 0.53-NT HIT: M29428.1, EVALUE 1.00e-120-SWISSPROT HIT: P08183, EVALUE 2.00e-27"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAAACCGTGAATCCTA 25
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DB 143 AGCTTCCAAACCGTGAATCCTA 119

RESULT 14
CQ308221/c
LOCUS Sequence 19326 from Patent WO0186003.
DEFINITION CQ308221
ACCESSION CQ308221.1 GI:41268798
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human lung
JOURNAL Patent: WO 0186003-A 19326 15-NOV-2001;
Aeomica, Inc. (US)

FEATURES
source location/Qualifiers
1..219
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002457.1-EXPRESSED IN LUNG, SIGNAL = 0.42-NT HIT: M29428.1, EVALUE 1.00e-120-SWISSPROT HIT: P08183, EVALUE 2.00e-27"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAAACCGTGAATCCTA 25
|||||
DB 143 AGCTTCCAAACCGTGAATCCTA 119

RESULT 15
CQ345026/c
LOCUS Sequence 19120 from Patent WO0157275.
DEFINITION CQ345026
ACCESSION CQ345026.1 GI:41294097
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
AUTHORS Human genome-derived single exon nucleic acid probes useful for
TITLE analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 19120 09-AUG-2001;
Aeomica, Inc. (US)

FEATURES
source location/Qualifiers
1..219
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002457.1-EXPRESSED IN BRAIN, SIGNAL = 0.57-NT HIT: M29428.1, EVALUE 1.00e-120-SWISSPROT HIT: P08183, EVALUE 2.00e-27"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAAACCGTGAATCCTA 25
|||||
DB 143 AGCTTCCAAACCGTGAATCCTA 119

Search completed: February 9, 2005, 17:02:00
Job time : 483.178 secs

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Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGTAATCCTA 25
Db 763 AGCTTCAACCAACGCTGTAATCCTA 739

RESULT 3

US-09-762-195-1/c
Sequence 1, Application US/09762195
Patent No. 6677319
GENERAL INFORMATION:
APPLICANT: Strommel, Wolfgang
TITLE OF INVENTION: Phosphatidylcholine as Medication with
FILE REFERENCE: 34691/208520
CURRENT APPLICATION NUMBER: US/09/762,195
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/EP9702426
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 198 57 570.8 DE
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3988
TYPE: DNA
ORGANISM: Homo sapiens
US-09-762-195-1

Query Match 100.0%; Score 25; DB 4; Length 3988;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGTAATCCTA 25
Db 710 AGCTTCAACCAACGCTGTAATCCTA 686

RESULT 4
US-09-672-810-1/c
Sequence 1, Application US/09672810
Patent No. 6617450
GENERAL INFORMATION:
APPLICANT: STOCKER, PENNY J.
APPLICANT: STEIMEL-CRESPI, DOROTHY T.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 4186
TYPE: DNA
ORGANISM: Macaca fascicularis
FEATURE:
NAME/KEY: CDS
LOCATION: (100)...(3940)
US-09-672-810-1

Query Match 100.0%; Score 25; DB 4; Length 4186;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGTAATCCTA 25
Db 740 AGCTTCAACCAACGCTGTAATCCTA 716

RESULT 5
US-09-672-810-3/c
Sequence 3, Application US/09672810
Patent No. 6617450
GENERAL INFORMATION:
APPLICANT: STOCKER, PENNY J.
APPLICANT: STEIMEL-CRESPI, DOROTHY T.
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 4195
TYPE: DNA
ORGANISM: Macaca fascicularis
FEATURE:
NAME/KEY: CDS
LOCATION: (100)...(3949)
US-09-672-810-3

Query Match 100.0%; Score 25; DB 4; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCAACCAACGCTGTAATCCTA 25
Db 749 AGCTTCAACCAACGCTGTAATCCTA 725

RESULT 6
US-08-784-649A-1/c
Sequence 1, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: SIKIC, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070

TELEFAX: 415-854-0875
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4264 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-784-649A-1

Query Match 100.0%; Score 25; DB 2; Length 4264;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCTA 25
 Db 779 AGCTTCCACACGCTGTAATCCTA 755

RESULT 7
 US-08-784-649A-5/c
 Sequence 5, Application US/08784649A
 Patent No. 5830697
 GENERAL INFORMATION:
 APPLICANT: SIKIC, Branimir I
 TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
 TITLE OF INVENTION: CYCLOSPORIN MODULATION
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 2200 Sand Hill Road
 CITY: Menlo Park
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/784,649A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sherwood, Pamela J
 REGISTRATION NUMBER: Reg.No. 5830697 36,677
 REFERENCE/DOCKET NUMBER: 06037/007001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-322-5070
 TELEFAX: 415-854-0875
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4264 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-784-649A-5

Query Match 100.0%; Score 25; DB 2; Length 4264;
 Best Local Similarity 100.0%; Pred. No. 0.0098;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCTA 25
 Db 779 AGCTTCCACACGCTGTAATCCTA 755

RESULT 8
 US-08-181-471-2/c
 Sequence 2, Application US/08181471

Patent No. 5641508
 GENERAL INFORMATION:
 APPLICANT: Li, Lingna
 APPLICANT: Lishko, Valeryi K.
 TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
 TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Thomas Fitting
 STREET: 12526 High Bluff Drive, Suite 300
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92130

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/181,471
 FILING DATE: 13-JAN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/041,553
 FILING DATE: 02-APR-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: ANT0029P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-792-3680
 TELEFAX: 619-792-8477

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4646 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:

NAME/KEY: CDS
 LOCATION: 425..4267
 US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;
 Best Local Similarity 100.0%; Pred. No. 0.0099;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCTA 25
 Db 1065 AGCTTCCACACGCTGTAATCCTA 1041

RESULT 9
 US-09-023-655-1167/c
 Sequence 1167, Application US/09023655
 Patent No. 6607879
 GENERAL INFORMATION:
 APPLICANT: Cocks, Benjamin G.
 APPLICANT: Susan G. Stuart
 APPLICANT: Jeffrey J. Seilhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 TITLE OF INVENTION: EXPRESSION
 NUMBER OF SEQUENCES: 1508
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1167:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187468
US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGGTGAATCCTA 25
Db 1065 AGCTTCACACCGGTGAATCCTA 1041

RESULT 10
US-08-583-276-18/c
Sequence 18, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
APPLICANT: McDonagh, Kevin T.
ATTORNEY/AGENT INFORMATION:
APPLICANT: Nienhuis, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994

APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 bases
TYPE: nucleic acid
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: Genomic DNA
US-08-583-276-18

Query Match 100.0%; Score 25; DB 2; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGGTGAATCCTA 25
Db 1065 AGCTTCACACCGGTGAATCCTA 1041

RESULT 11
US-08-752-447-1/c
Sequence 1, Application US/08752447
Patent No. 5994088
GENERAL INFORMATION:
APPLICANT: Mechetner, Eugene
ATTORNEY/AGENT INFORMATION:
APPLICANT: Robinson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,447
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5994088nam, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-08-752-447-1

Query Match 100.0%; Score 25; DB 2; Length 4669;

Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCTTCCACACGCTGTAATCCTA 25
Db 1065 AGCTTCCACACGCTGTAATCCTA 1041

RESULT 12
US-09-316-167-1/c
Sequence 1, Application US/09316167
Patent No. 635357
GENERAL INFORMATION:
APPLICANT: Mechetter, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316.167
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752.447
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. 636357nan, Kevin E
REGISTRATION NUMBER: 35.303
REFERENCE/DOCKET NUMBER: 95.1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-09-316-167-1

Query Match 100.0%; Score 25; DB 3; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCTTCCACACGCTGTAATCCTA 25
Db 1065 AGCTTCCACACGCTGTAATCCTA 1041

RESULT 13
US-09-397-233-1/c

Sequence 1, Application US/09397233
Patent No. 6630327
GENERAL INFORMATION:
APPLICANT: Mechetter, Eugene
APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Methods and Reagents for Preparing and
Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397.233
FILING DATE: 16-Sep-1999
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: No. 6630327nan, Kevin E
REGISTRATION NUMBER: 35.303
REFERENCE/DOCKET NUMBER: 95.1121-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA

FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424

FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264

FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-397-233-1

Query Match 100.0%; Score 25; DB 4; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGCTTCCACACGCTGTAATCCTA 25
Db 1065 AGCTTCCACACGCTGTAATCCTA 1041

RESULT 14
5206352-3/c

Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
Michael M.

TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622.836
FILING DATE: 24-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892.575
FILING DATE: 01-AUG-1986

; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO:3
; LENGTH: 4669
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCACGCTGAATCCTA 25
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Db 1065 AGCTTCCACCACGCTGAATCCTA 1041

RESULT 15
5206352-3/C
; Patent No. 5206352
; APPLICANT: Roninson, Igor B.; Pastan, Ira H.; Gottesman,
; Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/622,836
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 892,575
; FILING DATE: 01-AUG-1986
; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO:3
; LENGTH: 4669
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCACGCTGAATCCTA 25
|||
Db 1065 AGCTTCCACCACGCTGAATCCTA 1041

Search completed: February 9, 2005, 17:11:17
Job time: 79.592 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds
(Without alignments)
539.601 Million cell updates/sec

Title: US-10-007-255-12
Perfect score: 25
Sequence: 1 agcttccaccacggtgaatcccta 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	172	9	US-09-864-761-27462
2	25	100.0	209	15	US-10-101-510-284
3	25	100.0	219	9	US-09-864-761-27770
4	25	100.0	463	9	US-09-864-761-10820
5	25	100.0	473	9	US-09-864-761-11142
6	25	100.0	2307	9	US-09-805-020-31
7	25	100.0	3840	18	US-10-384-339C-30
8	25	100.0	3852	15	US-10-101-433A-1
9	25	100.0	3860	9	US-09-866-866A-1
10	25	100.0	3860	9	US-09-866-866A-3
11	25	100.0	4186	17	US-10-619-359A-1

12	25	100.0	4195	17	US-10-619-359A-3	Sequence 3, Appli
13	25	100.0	4533	9	US-09-805-020-30	Sequence 30, Appli
14	25	100.0	4643	13	US-10-072-621-2	Sequence 2, Appli
15	25	100.0	4643	14	US-10-097-340-1	Sequence 1, Appli
16	25	100.0	4643	15	US-10-007-926A-258	Sequence 258, App
17	25	100.0	4646	11	US-09-968-007A-459	Sequence 459, App
18	25	100.0	4646	11	US-09-968-007A-459	Sequence 747, App
19	25	100.0	4646	17	US-09-968-007A-747	Sequence 1167, Ap
20	25	100.0	4646	17	US-10-641-643-1167	Sequence 1, Appli
21	25	100.0	4646	17	US-10-343-657-1	Sequence 198, App
22	25	100.0	4646	18	US-10-775-169-198	Sequence 1, Appli
23	25	100.0	4669	18	US-10-680-516-1	Sequence 1, Appli
24	25	100.0	8630	9	US-09-306-417-1	Sequence 2, Appli
25	25	100.0	8630	9	US-09-306-417-2	Sequence 5, Appli
26	21.8	87.2	4254	9	US-09-866-866A-5	Sequence 1424, Ap
27	21.8	87.2	4254	17	US-10-388-934-265	Sequence 265, App
28	21.8	87.2	4254	17	US-10-152-319A-1484	Sequence 1484, Ap
29	21.8	87.2	4298	18	US-10-335-053-32	Sequence 32, Appli
30	21.8	87.2	4788	9	US-09-866-866A-7	Sequence 7, Appli
31	20.2	80.8	4317	13	US-10-739-930-4420	Sequence 4420, Ap
32	20.2	80.8	4317	13	US-10-044-671-1	Sequence 1, Appli
33	20.2	80.8	4317	18	US-10-896-434-1	Sequence 1, Appli
34	20.2	80.8	4317	18	US-10-896-434-1	Sequence 1, Appli
35	20.2	80.8	4359	9	US-09-769-097-3	Sequence 355, App
36	19.2	76.8	71251	13	US-10-087-192-355	Sequence 40, Appli
37	18.6	74.4	44377	17	US-10-085-117-40	Sequence 160, App
38	18.6	74.4	94720	17	US-10-052-482-160	Sequence 2953, Ap
39	18.2	72.8	325	18	US-10-425-115-2953	Sequence 445, Appli
40	18.2	72.8	22644	13	US-10-087-192-445	Sequence 26719, A
41	17.8	71.2	451	17	US-10-425-599-26719	Sequence 26721, A
42	17.6	70.4	451	17	US-10-424-599-26721	Sequence 994, App
43	17.6	70.4	1792	17	US-10-087-192-994	Sequence 1165, Ap
44	17.6	70.4	50002	13	US-10-087-192-994	
45	17.6	70.4	100554	13	US-10-087-192-1165	

ALIGNMENTS

RESULT 1
US-09-864-761-27462
Sequence 27462, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aesomica-X-1
CURRENT APPLICATION NUMBER: US/09/864, 761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27462
LENGTH: 172
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005068.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.64
OTHER INFORMATION: SWISSPROT HIT: P08183, EVALUE 3.00e-27
OTHER INFORMATION: NT HIT: AF016535.1, EVALUE 2.00e-92
OTHER INFORMATION: EST_HUMAN HIT: AW847648.1, EVALUE 2.30e+00
US-09-864-761-27462

Query Match 100.0%; Score 25; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCCAACCAACGCTGTAATCCTA 25
DB 62 AGCTCCAACCAACGCTGTAATCCTA 86

RESULT 2
US-10-101-510-284/c
Sequence 284, Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 284
LENGTH: 209
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-284

Query Match 100.0%; Score 25; DB 15; Length 209;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCCAACCAACGCTGTAATCCTA 25
DB 204 AGCTCCAACCAACGCTGTAATCCTA 180

RESULT 3
US-09-864-761-27770/c
Sequence 27770, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27770
LENGTH: 219
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC002457.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57
OTHER INFORMATION: NT HIT: M29428.1, EVALUE 1.00e-120
OTHER INFORMATION: SWISSPROT HIT: P08183, EVALUE 2.00e-27
US-09-864-761-27770

Query Match 100.0%; Score 25; DB 9; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCCAACCAACGCTGTAATCCTA 25
DB 143 AGCTCCAACCAACGCTGTAATCCTA 119


```

RESULT 4
US-09-864-761-10820
; Sequence 10820, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT FILING DATE: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10820
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005068.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.64
US-09-864-761-10820

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Query Match          100.0%; Score 25; DB 9; Length 463;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCTTCAACCAACGCTGTAATCCTA 25
Db 340 AGCTTCAACCAACGCTGTAATCCTA 364

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```

RESULT 5
US-09-864-761-11142/c
; Sequence 11142, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT FILING DATE: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11142
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002457.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57
US-09-864-761-11142

```

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Query Match          100.0%; Score 25; DB 9; Length 473;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCTTCAACCAACGCTGTAATCCTA 25
Db 404 AGCTTCAACCAACGCTGTAATCCTA 380

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RESULT 6
US-09-805-020-31/c
; Sequence 31, Application US/09805020
; Publication No. US20020085384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805.020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(2307)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-31

Query Match 100.0%; Score 25; DB 9; Length 2307;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCAACACGCTGTAATCCTA 25
DB 1065 AGCTTCAACACGCTGTAATCCTA 1041

RESULT 7
US-10-384-339C-30/c
; Sequence 30, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzler, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GENE
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384.339C
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 3840
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: mdt-1
; PATENT DOCUMENT NUMBER: AP016535
US-10-384-339C-30

Query Match 100.0%; Score 25; DB 18; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCAACACGCTGTAATCCTA 25
DB 641 AGCTTCAACACGCTGTAATCCTA 617

RESULT 8

US-10-101-433A-1/c
; Sequence 1, Application US/10101433A
; Publication No. US20030119726A1
; GENERAL INFORMATION:
; APPLICANT: Hanscom, Sara
; APPLICANT: Crespi, Charles
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307/70019
; CURRENT APPLICATION NUMBER: US/10/101.433A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/277.095
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3852
; TYPE: DNA
; ORGANISM: Macaca mulatta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3852)
US-10-101-433A-1

Query Match 100.0%; Score 25; DB 15; Length 3852;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCAACACGCTGTAATCCTA 25
DB 650 AGCTTCAACACGCTGTAATCCTA 626

RESULT 9
US-09-866-866A-1/c
; Sequence 1, Application US/09866866A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-02CIR2
; CURRENT APPLICATION NUMBER: US/09/866.866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-866A-1

Query Match 100.0%; Score 25; DB 9; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCAACACGCTGTAATCCTA 25
DB 641 AGCTTCAACACGCTGTAATCCTA 617

RESULT 10
US-09-866-866A-3/c
; Sequence 3, Application US/09866866A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John

```

; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 3
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-866-866A-3

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Query Match      100.0%; Score 25; DB 9; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGCTTCAACCAACGCTGTAATCCTA 25
Db      641 AGCTTCAACCAACGCTGTAATCCTA 617

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RESULT 11

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; Sequence 1, Application US/10619359A
; Publication No. US20040077000A1
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307.70020.US
; CURRENT APPLICATION NUMBER: US/10/619,359A
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 09/672,810
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 4186
; TYPE: DNA
; ORGANISM: Macaca fascicularis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(3940)
; US-10-619-359A-1

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Query Match      100.0%; Score 25; DB 17; Length 4186;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGCTTCAACCAACGCTGTAATCCTA 25
Db      740 AGCTTCAACCAACGCTGTAATCCTA 716

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RESULT 12

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; Sequence 3, Application US/10619359A
; Publication No. US20040077000A1
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.

```

```

; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307.70020.US
; CURRENT APPLICATION NUMBER: US/10/619,359A
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 09/672,810
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 4195
; TYPE: DNA
; ORGANISM: Macaca fascicularis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)...(3949)
; US-10-619-359A-3

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Query Match      100.0%; Score 25; DB 17; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGCTTCAACCAACGCTGTAATCCTA 25
Db      749 AGCTTCAACCAACGCTGTAATCCTA 725

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RESULT 13

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; Sequence 30, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zuric
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 30
; LENGTH: 4533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(4533)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
; US-09-805-020-30

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Query Match      100.0%; Score 25; DB 9; Length 4533;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 AGCTTCAACCAACGCTGTAATCCTA 25
Db      1065 AGCTTCAACCAACGCTGTAATCCTA 1041

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RESULT 14

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; Sequence 2, Application US/10072621
; Publication No. US20020169137A1
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Conop, Bruce P.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
; FILE REFERENCE: 100103.402
; CURRENT APPLICATION NUMBER: US/10/072,621

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;; CURRENT FILING DATE: 2002-02-08
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 4643
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-072-621-2

Query Match 100.0%; Score 25; DB 13; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACGCTGAATCCTA 25
DB 1065 AGCTTCCACCAACGCTGAATCCTA 1041

RESULT 15
US-10-097-340-1/c
; Sequence 1, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNANVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-1

Query Match 100.0%; Score 25; DB 14; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACCAACGCTGAATCCTA 25
DB 1065 AGCTTCCACCAACGCTGAATCCTA 1041

Search completed: February 9, 2005, 22:26:39
Job time : 267.667 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds
(without alignment) 602.360 Million cell updates/sec

Title: US-10-007-255-12

Perfect score: 1 agcttcaccacacgtgaactcta 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_GeneSeq_16Dec04:*
1: geneSeq1980s:*
2: geneSeq1990s:*
3: geneSeq2000s:*
4: geneSeq2001as:*
5: geneSeq2001bs:*
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7: geneSeq2002bs:*
8: geneSeq2003as:*
9: geneSeq2003bs:*
10: geneSeq2003cs:*
11: geneSeq2003ds:*
12: geneSeq2004as:*
13: geneSeq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	25	100.0	25	6	AAD39011 Human mdr
C 2	25	100.0	25	6	AAD39001 Human mdr
C 3	25	100.0	120	6	ABK87742 Multiple
C 4	25	100.0	120	6	ABK87743 Multiple
C 5	25	100.0	172	4	AA150383 Probe #19
C 6	25	100.0	172	4	AA44387 Human bon
C 7	25	100.0	172	4	AAK18477 Human bra
C 8	25	100.0	172	4	AB44044 Human liv
C 9	25	100.0	172	6	AB518622 Human gen
C 10	25	100.0	209	6	AB235172 Human gen
C 11	25	100.0	219	4	AAK45086 Human bon
C 12	25	100.0	219	4	AAK19129 Human bra
C 13	25	100.0	219	6	AB19335 Human gen
C 14	25	100.0	463	4	AA137193 Probe #58
C 15	25	100.0	463	4	AAK31296 Human bon
C 16	25	100.0	463	4	AAK05682 Human bra
C 17	25	100.0	463	4	AB530977 Human liv
C 18	25	100.0	463	6	AB506048 Human gen
C 19	25	100.0	473	4	AAK32026 Human bon
C 20	25	100.0	473	4	AAK06359 Human bra

C 21	25	100.0	473	6	AB506792	Ab506792 Human gen
C 22	25	100.0	807	1	AAAT0751	AAAT0751 Sequence
C 23	25	100.0	2307	6	AB565230	AB565230 cDNA enco
C 24	25	100.0	3840	6	ABV78146	ABV78146 Human mdr
C 25	25	100.0	3840	6	AB235722	AB235722 Human mdr
C 26	25	100.0	3840	6	ABX09965	ABX09965 Human mdr
C 27	25	100.0	3840	6	ABL91687	ABL91687 Human pol
C 28	25	100.0	3843	6	ABO78185	ABO78185 Human MDR
C 29	25	100.0	3852	8	ABT14496	ABT14496 Rhesus mo
C 30	25	100.0	3860	3	AAZ49332	AAZ49332 Human wil
C 31	25	100.0	3860	3	AAZ49333	AAZ49333 Human G18
C 32	25	100.0	3860	6	ABA94365	ABA94365 Human BCR
C 33	25	100.0	3860	6	ABA94366	ABA94366 Human BCR
C 34	25	100.0	3988	3	AAZ88973	AAZ88973 Human MDR
C 35	25	100.0	4186	4	AAZ86127	AAZ86127 Cynomolog
C 36	25	100.0	4195	4	AAZ86128	AAZ86128 Mutated h
C 37	25	100.0	4264	2	AAV6553	AAV6553 Mutated h
C 38	25	100.0	4264	2	AAV6554	AAV6554 Mutated h
C 39	25	100.0	4349	4	AAH57442	AAH57442 Human int
C 40	25	100.0	4378	2	AAO04522	AAO04522 Multidrug
C 41	25	100.0	4533	6	AB565229	AB565229 cDNA enco
C 42	25	100.0	4643	6	ABV76368	ABV76368 cDNA enco
C 43	25	100.0	4643	6	ABV94267	ABV94267 Breast ca
C 44	25	100.0	4643	6	ABV74349	ABV74349 Human ABC
C 45	25	100.0	4643	10	ABX77217	ABX77217 cDNA enco

ALIGNMENTS

RESULT 1	AAAD39011/C	AAAD39011 standard; DNA, 25 BP.
ID	AAAD39011	standard; DNA, 25 BP.
XX	AC	AAAD39011;
XX	AC	AAAD39011;
DT	23-SEP-2002	(first entry)
XX	Human mdr1 gene	HIF-1 binding site DNA #4.
DE	Human	hematologic malignancy; multidrug resistance; MDR; SUMO-1;
XX	Human	hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;
KW	Human	lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
KW	Human	myeloid disorder; lymphocytic leukaemia; thrombocythemia; myeloma;
KW	Human	angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;
KW	Human	polycythemia vera; hypoxia responsive element; HRE; ds.
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	misc_binding	11..15
FT	/*leg= a	/bound_molety= "HIF-1"
FT		
XX	WO200234291-A2.	
XX	02-MAY-2002.	
PD	25-OCT-2001; 2001WO-US049856.	
XX	26-OCT-2000; 2000US-0243542P.	
PR	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.	
XX	Colgan SP;	
XX	WPI; 2002-471427/50.	
DR	Treating a subject (at risk of) having a hematologic malignancy or	
PT	multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia	
PT	inducible factor 1 binding molecules or small ubiquitin-like-modifier-1	
PT	binding molecules.	
XX		

PS Example 2; Page 12; 92pp; English.

XX The invention relates to a method of treating a subject having or at risk

CC of developing a haematologic malignancy or multidrug resistance (MDR).

CC The method involves administering hypoxia inducible factor-1 (HIF-1)

CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding

CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive

CC element (HRE) binding molecules or antisense nucleic acid molecules and

CC SUMO-1 binding molecules or antisense molecules are useful for treating a

CC subject having or at risk of developing haematologic malignancy or MDR

CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders

CC include lymphocytic leukaemia or chronic lymphoproliferative disorders

CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid

CC disorders include chronic or acute myeloid leukaemia, e.g. angioleukemia

CC myeloid metaplasia, essential thrombocythemia or polycythemia vera. The

CC invention is used in gene therapy. The present sequence is human mdr1

CC gene HIF-1 binding site DNA

XX

SQ Sequence 25 BP; 6 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAAACGCGTGAATCCTA 25

Db 25 AGCTTCCAAACGCGTGAATCCTA 1

RESULT 2

AAD39001 standard; DNA; 25 BP.

AC AAD39001;

XX 23-SEP-2002 (first entry)

XX Human mdr1-HRE antisense oligonucleotide #4.

XX

XX Human haematologic malignancy; multidrug resistance; MDR; SUMO-1;

XX hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;

XX lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;

XX myeloid disorder; lymphocytic leukaemia; thrombocythemia; myeloma;

XX angioleukemia; myeloid metaplasia; myeloid leukaemia; gene therapy;

XX polycythemia vera; hypoxia responsive element; HRE; antisense;

XX phosphorothioate backbone; ss.

OS Homo sapiens.

OS Synthetic.

OS

XX Key Location/Qualifiers

XX modified_base 1..25

XX /*tag= a

XX /mod_base= OTHER

XX /note= "Phosphorothioate backbone"

XX

XX WO200234291-A2.

XX

XX 02-MAY-2002.

XX

XX 25-OCT-2001; 2001WO-US049856.

XX

XX 26-OCT-2000; 2000US-0243542P.

XX

XX (BGM) BRIGHAM & WOMENS HOSPITAL INC.

XX Colgan SP;

XX WPI; 2002-471427/50.

XX

XX Treating a subject (at risk of) having a haematologic malignancy or

XX multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

XX inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

PT

PT binding molecules.

XX

XX Claim 14; Page 43; 92pp; English.

XX

CC The invention relates to a method of treating a subject having or at risk

CC of developing a haematologic malignancy or multidrug resistance (MDR).

CC The method involves administering hypoxia inducible factor-1 (HIF-1)

CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding

CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive

CC element (HRE) binding molecules or antisense nucleic acid molecules and

CC SUMO-1 binding molecules or antisense molecules are useful for treating a

CC subject having or at risk of developing haematologic malignancy or MDR

CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders

CC include lymphocytic leukaemia or chronic lymphoproliferative disorders

CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid

CC disorders include chronic or acute myeloid leukaemia, e.g. angioleukemia

CC myeloid metaplasia, essential thrombocythemia or polycythemia vera. The

CC invention is used in gene therapy. The present sequence is an antisense

CC oligo targeted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its

CC expression. This oligo is used in the exemplification of the invention

XX

SQ Sequence 25 BP; 8 A; 8 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAAACGCGTGAATCCTA 25

Db 1 AGCTTCCAAACGCGTGAATCCTA 25

RESULT 3

ABK87742/C

ID ABK87742 standard; DNA; 120 BP.

XX

XX ABK87742;

XX

XX 07-OCT-2002 (first entry)

XX

XX Multiple drug resistance gene, MDR1, sequence #3.

XX

XX MDR1; dr; multiple drug resistance gene; nucleic acid amplification;

XX MDR1 expression level; multiple drug resistance.

XX

XX Unidentified.

OS

XX JP2002153274-A.

XX

XX 28-MAY-2002.

XX

XX 17-NOV-2000; 2000JP-00351224.

XX

XX 17-NOV-2000; 2000JP-00351224.

XX

XX (KAIN-) KAINOSU KK.

XX

XX WPI; 2002-552738/59.

XX

XX A primer for amplifying a nucleic acid comprises a specific

XX oligonucleotide sequence for determination of Multiple Drug Resistance

XX gene expression level by nucleic acid amplification.

XX

XX Claim 7; Page 6; 7pp; Japanese.

XX

XX The invention relates to a primer for amplifying a nucleic acid

XX comprising a 15 to 30 base continuous oligonucleotides of an MDR1

XX (multiple drug resistance gene 1) gene fragment appearing as ABK87740.

XX Also included are a kit for quantitatively determining the expression

XX level of MDR1 gene, a probe for capturing a nucleic acid, a reagent for

XX amplifying a nucleic acid and diagnosis of the drug resistance of a

XX patient. The primer is useful for the determination of MDR expression

XX level by nucleic acid amplification. The present sequence is a fragment

CC

CC of the MDR1 gene
 XX Sequence 120 BP; 28 A; 21 C; 27 G; 44 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 25; DB 6; Length 120;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCCACACGCTGTAATCCTA 25
 |||||
 DB 79 AGCTTCCACACGCTGTAATCCTA 55

RESULT 4
 ABK87743
 ID ABK87743 standard; DNA; 120 BP.
 AC ABK87743;
 XX
 XX 07-OCT-2002 (first entry)
 DT
 XX
 DE Multiple drug resistance gene, MDR1, sequence #4.
 XX
 KM MDR1; drg, multiple drug resistance gene; nucleic acid amplification;
 KM MDR1 expression level; multiple drug resistance.
 XX
 OS Unidentified.
 XX
 PN JP2002153274-A.
 PD
 XX 28-MAY-2002.
 PF
 XX 17-NOV-2000; 2000JP-00351224.
 PR
 XX 17-NOV-2000; 2000JP-00351224.
 PA (KAIN-) KAINOSU KK.
 XX
 XX WPI; 2002-552736/59.
 DR
 XX
 PT A primer for amplifying a nucleic acid comprises a specific
 PT oligonucleotide sequence for determination of Multiple Drug Resistance
 PT gene expression level by nucleic acid amplification.
 XX
 PS Claim 9; Page 6; 7pp; Japanese.
 XX
 CC The invention relates to a primer for amplifying a nucleic acid
 CC comprising a 15 to 30 base continuous oligonucleotide of an MDR1
 CC (multiple drug resistance gene 1) gene fragment appearing as ABK87740.
 CC Also included are a kit for quantitatively determining the expression
 CC level of MDR1 gene, a probe for capturing a nucleic acid, a reagent for
 CC amplifying a nucleic acid and diagnosis of the drug resistance of a
 CC patient. The primer is useful for the determination of MDR expression
 CC level by nucleic acid amplification. The present sequence is a fragment
 CC of the MDR1 gene
 CC
 XX
 SQ Sequence 120 BP; 44 A; 27 C; 21 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 120;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCCACACGCTGTAATCCTA 25
 |||||
 DB 42 AGCTTCCACACGCTGTAATCCTA 66

RESULT 5
 AA150383
 ID AA150383 standard; DNA; 172 BP.
 AC AA150383;
 XX

DT 17-OCT-2001 (first entry)
 XX
 DE Probe #19069 used to measure gene expression in human placenta sample.
 XX
 KM Probe; microarray; human; placenta; antenatal diagnosis;
 KM genetic disorder; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO200157272-A2.
 PN
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000663.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-0063366P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX WPI; 2001-48897/53.
 DR
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX
 PS Claim 25; SEQ ID NO 19069; 654bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders
 CC
 XX
 SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 4; Length 172;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTTCCACACGCTGTAATCCTA 25
 |||||
 DB 62 AGCTTCCACACGCTGTAATCCTA 86

RESULT 6
 AAK44387
 ID AAK44387 standard; DNA; 172 BP.
 AC AAK44387;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed single exon probe SEQ ID NO: 18944.
 XX
 KM Human; bone marrow expressed exon; gene expression analysis; probe;
 KM microarray; cancer; leukaemia; lymphoma; myeloma; ss.
 OS
 XX Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 XX 09-AUG-2001.
 PD
 XX 30-JAN-2001; 2001WO-US000668.
 PF
 XX 04-FEB-2000; 2000US-0180312P.
 PR

```

PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 18944; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTTCCACACGCTGTAATCCTA 25
DB 62 AGCTTCCACACGCTGTAATCCTA 86
XX
RESULT 7
AAK18477
ID AAK18477 standard; DNA; 172 BP.
XX
AC AAK18477;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 18468.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human

```

```

PT brains.
XX
XX Example 4; SEQ ID NO 18468; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTTCCACACGCTGTAATCCTA 25
DB 62 AGCTTCCACACGCTGTAATCCTA 86
XX
RESULT 8
ABS44044
ID ABS44044 standard; DNA; 172 BP.
XX
AC ABS44044;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID NO 19034.
XX
KW Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488998/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
PS Claim 4; SEQ ID NO 19034; 658bp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (1) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (1) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is

```


CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCTTCCACACGCTGTAATCCCA 25
62 AGCTTCCACACGCTGTAATCCCA 86
Db
RESULT 9
ABS18622 standard, DNA; 172 BP.
XX
XX ABS18622;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human genome-derived single exon probe ORF from lung SEQ ID NO 18613.
DE
XX
XX Human; de; single exon probe; asthma; lung cancer; COPD; ILD;
XX chronic obstructive pulmonary disease; interstitial lung disease;
XX familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome;
XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
XX primary ciliary dyskinesia; pulmonary hypertension;
XX hyaline membrane disease; open reading frame; ORF.
KM
XX
XX Homo sapiens.
OS
XX
XX W0200186003-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000665.
PF
XX
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX
XX WPI, 2002-114183/15.
DR
XX
XX Spatially-addressable set of single exon nucleic acid probes, used to
XX measure gene expression in human lung samples.
PT
XX
XX Claim 4; SEQ ID NO 18613; 634bp; English.
XX
XX
XX The invention relates to a spatially-addressable set of single exon
XX nucleic acid probes for measuring gene expression in a sample derived
XX from human lung comprising single exon nucleic acid probes having one of
XX 12614 nucleic acid sequences mentioned in the specification, or their
XX complements or the 12387 open reading frames derived from the 12614
XX probes. Also included are a microarray comprising the novel set of probes
XX; the novel set of probes which hybridise at high stringency to a nucleic
XX acid expressed in the human lung; measuring gene expression in a sample
XX derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA; and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis; and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Kartagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 172 BP; 58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGCTTCCACACGCTGTAATCCCA 25
62 AGCTTCCACACGCTGTAATCCCA 86
Db

RESULT 10
AB235172/c
ID AB235172 standard; cDNA; 209 BP.
XX
XX
XX ABS235172;
AC
XX
XX 05-FEB-2003 (first entry)
DT
XX
XX Human gene expression profile polynucleotide SEQ ID NO 284.
DE
XX
XX Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
XX bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
XX tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
XX gene expression; gene; ss.
KM
XX
XX Homo sapiens.
OS
XX
XX W0200274979-A2.
PN
XX
XX 26-SEP-2002.
PD
XX
XX 20-MAR-2002; 2002WO-US008456.
PF
XX
XX 20-MAR-2001; 2001US-0276947P.
PR
XX
XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
PA
XX
XX Wan J, Wang Y;
PI
XX
XX WPI, 2002-740862/80.
DR
XX
XX New gene expression profile generated from primary, endothelial,
PT

PT epithelial, and muscle cell types, useful for identifying disease
 PT pathologies involving alterations of gene expression, e.g. cancer.
 XX
 PS Claim 10; Page 448; 850bp; English.

CC The invention relates to a gene expression profile comprising one or more
 CC genes (AB23489-AB235692) and generated from a cell type. The cell type
 CC is a coronary artery endothelium, umbilical artery or vein endothelium,
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
 CC endothelium, myometrium microvascular endothelium, keratinocyte
 CC epithelium, bronchial epithelium, mammary epithelium, prostate
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
 CC small airway epithelium, renal epithelium, umbilical artery smooth
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
 CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
 CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
 CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
 CC osteoblasts or prostate stromal cell. The gene expression profile is used
 CC for determining the level of RNA expression for a sample, determining the
 CC phenotype of a cell and distinguishing cell types. The gene or a protein
 CC expression profile is useful in identifying disease pathologies involving
 CC alterations of gene expression. The assessment of expression profiles may
 CC provide meaningful information with respect to tumour type and stage,
 CC treatment methods, and prognosis. The gene or protein expression profile
 CC may also be used for creating microarrays. The microarray is useful for
 CC genetic and physical mapping of genomes, DNA sequencing, genetic or
 CC medical diagnosis, genotyping of organisms, confirming cell or tissue
 CC identifications and in identifying promising antibiotics, antiviral or
 CC antifungal agents

XX SQ Sequence 209 BP; 65 A; 39 C; 38 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 209;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACACGCTGTAATCCTA 25
 |||||
 Db 204 AGCTTCCACACGCTGTAATCCTA 180

RESULT 11
 AAK45086/c
 ID AAK45086 standard; DNA; 219 BP.

XX AAK45086;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 19643.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KM microarray; cancer; leukemia; lymphoma; myeloma; ss.

XX Homo sapiens.

XX MO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.

XX Example 4; SEQ ID NO 19643; 658bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is one of
 CC the probes of the invention

XX SQ Sequence 219 BP; 54 A; 38 C; 51 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 4; Length 219;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCACACGCTGTAATCCTA 25
 |||||
 Db 143 AGCTTCCACACGCTGTAATCCTA 119

RESULT 12
 AAK19129/c
 ID AAK19129 standard; DNA; 219 BP.

XX AAK19129;

XX 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe SEQ ID NO: 19120.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;
 KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
 KM ss.

XX Homo sapiens.

XX MO200157275-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000667.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.

XX Example 4; SEQ ID NO 19120; 650bp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the

CC invention
XX sequence 219 BP; 54 A; 38 C; 51 G; 76 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 25; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTTCCACCACGCTGTAATCCTA 25
Db 143 AGCTTCCACCACGCTGTAATCCTA 119
RESULT 13
ABS19335/C
ID ABS19335 standard; DNA; 219 BP.
XX
AC ABS19335;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 19326.
KW Human; der; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN MO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180332P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PD WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
measure gene expression in human lung samples.
XX
PS Claim 4; SEQ ID NO 19326; 634bp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human lung comprising single exon nucleic acid probes having one of
12614 nucleic acid sequences mentioned in the specification, or their
complements or the 12387 open reading frames derived from the 12614
probes. Also included are a microarray comprising the novel set of probes
; the novel set of probes which hybridise at high stringency to a nucleic
acid expressed in the human lung; measuring gene expression in a sample
derived from human lung, comprising (a) contacting the array with a
collection of detectably labeled nucleic acids derived from human lung
mRNA, and (b) measuring the label detectably bound to each probe of the
array; identifying exons in a eukaryotic genome, comprising (a)
algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray, assigning exons to a single gene.
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 219 BP; 54 A; 38 C; 51 G; 76 T; 0 U; 0 Other;
QY
Query Match 100.0%; Score 25; DB 6; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 143 AGCTTCCACCACGCTGTAATCCTA 119
1 AGCTTCCACCACGCTGTAATCCTA 25
AGCTTCCACCACGCTGTAATCCTA 119
RESULT 14
ID AAI37193 standard; DNA; 463 BP.
XX
AC AAI37193;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #5879 used to measure gene expression in human placenta sample.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180332P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PD WPI; 2001-48897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

XX Claim 25; SEQ ID NO 5879; 654bp; English.

CC The present invention relates to single exon nucleic acid probes (SENP).

CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders

XX SQ Sequence 463 BP; 153 A; 100 C; 98 G; 112 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 4; Length 463;

Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTTCCAACCCAGTGTAATCCTA 25

Db 340 AGCTTCCAACCCAGTGTAATCCTA 364

RESULT 15

AAK31296
ID AAK31296 standard; DNA; 463 BP.

AC AAK31296;

DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 5853.

KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

OS Homo sapiens.

XX MO200157276-A2.

XX 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

DR Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 5853; 658bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukemia and myeloma. The present sequence is one of

QY 1 AGCTTCCAACCCAGTGTAATCCTA 25

Db 340 AGCTTCCAACCCAGTGTAATCCTA 364

Search completed: February 9, 2005, 16:05:58
Job time: 247.69 secs

Query Match 100.0%; Score 25; DB 4; Length 463;

Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Sequence 463 BP; 153 A; 100 C; 98 G; 112 T; 0 U; 0 Other;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds
(without alignments)
388.593 Million cell updates/sec

Title: US-10-007-255-12

Perfect score: 25

Sequence: 1 agcttccaccacgctgaactccta 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1.*
2: gb_est2.*
3: gb_hlc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	3843	9	AY408954 Homo sapi
C 2	25	100.0	3843	9	AY408955 Pan trogl
C 3	21.8	87.2	3182	3	AK030328 Mus muscu
C 4	21.8	87.2	3816	9	AY408956 Mus muscu
C 5	20.8	83.2	682	7	CP176579 805414 MA
C 6	20.2	80.8	478	2	BE217416 fbn-1094
C 7	20.2	80.8	806	3	CNSOALN4
C 8	19.8	79.2	489	3	AZ957679 Arabidops
C 9	19.8	79.2	775	4	BI691631 603307314
C 10	19.8	76.8	526	8	BH521842 BOGOF607F
C 11	19.2	76.8	553	1	AU291400 AU291400
C 12	19.2	76.8	589	8	BH174634 B1F51B20
C 13	19.2	76.8	604	8	BH713924 BOMC1387F
C 14	19.2	76.8	617	8	BH696214 BOMNB047R
C 15	19.2	76.8	634	8	BH698731 BOMC1677F
C 16	19.2	76.8	652	8	AZ341385 IM0073B15
C 17	19.2	76.8	656	8	CC951154 BOMGM457F
C 18	19.2	76.8	657	8	BH983332 cdf102c02.
C 19	19.2	76.8	692	8	BZ010051 oej74907.
C 20	19.2	76.8	722	9	CC967311 BOIH637R
C 21	19.2	76.8	731	5	BO974293 OH15E03.
C 22	19.2	76.8	779	8	BZ427781 BONOA377R
C 23	19.2	76.8	783	8	BH480667 BOHC8447R
C 24	19.2	76.8	799	8	BH701776 BOME117F

25	19.2	76.8	804	8	BH600441
26	19.2	76.8	805	8	BH068818
27	19.2	76.8	840	8	BZ493588 BOMK207F
C 28	19.2	76.8	865	9	CC909091 t047p02ba
C 29	19.2	76.8	983	8	BZ501403 BOMK1597F
C 30	19.2	76.8	2239	3	AK090183 Mus muscu
C 31	18.8	75.2	732	9	AG425665 Mus muscu
C 32	18.8	75.2	1749	3	AK086811 Mus muscu
C 33	18.6	74.4	169	9	CE015031 tigr-g88-
C 34	18.6	74.4	173	9	CR063094 Forward 8
C 35	18.6	74.4	201	8	AZ001999 RPCT-23-3
C 36	18.6	74.4	233	9	CR055056 Forward 8
C 37	18.6	74.4	337	4	BI301745 UI-R-DL0-
C 38	18.6	74.4	337	4	BI301966 UI-R-DL0-
C 39	18.6	74.4	368	2	BB872680 BB872680
C 40	18.6	74.4	389	2	BF806551 PM2-C1005
C 41	18.6	74.4	412	2	BF805641 PM2-C1005
C 42	18.6	74.4	412	2	BF808478 PM2-C1005
C 43	18.6	74.4	483	8	BH858848 S3_x011c2
C 44	18.6	74.4	504	8	BH858849 S3_x011c2
C 45	18.6	74.4	528	1	AI965324 fc89h05.x

ALIGNMENTS

RESULT 1
AY408954/c 3843 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens ABCB1 gene, VIRUAL TRANSCRIPT, partial sequence,
LOCUS AY408954 GI:39764922
ACCESSION AY408954
VERSION AY408954.1 GI:39764922
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3843)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNML Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..3843
location/Qualifiers
/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="taxon:9606"
<1..3843
/gene="ABCB1"
/locus_tag="HGM3396"
ORIGIN
Query Match 100.0%; Score 25; DB 9; Length 3843;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTTCAACACCGTAAATCCTA 25
|||||

Db 641 AGCTCCACCGCTGTAATCCTA 617

RESULT 2
AY408955/c 3843 bp DNA linear GSS 15-DEC-2003
LOCUS Pan troglodytes ABCB1 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY408955 GI:39764923
VERSION GSS.
KEYWORDS Pan troglodytes (chimpanzee)
SOURCE Mammalia: Eutheria: Chordata: Craniata: Vertebrata: Euteleostomi:
ORGANISM Eukaryota: Eutheria: Primates: Catarrhini: Homiidae: Pan.
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Ciolek,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,D.J.,
Adams,M.D. and Cargill,M.
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous
gene tries
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS 2 (bases 1 to 3843)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Ciolek,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,D.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Glade Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..3843
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..31843
/gene="ABCB1"
/locus_tag="HCM3396"
ORIGIN
Query Match 100.0%; Score 25; DB 9; Length 3843;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCTCCACCGCTGTAATCCTA 25
Db 641 AGCTCCACCGCTGTAATCCTA 617
RESULT 3
AK030328/c 3182 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
DEFINITION RIKEN full-length enriched library, clone:5031438E12
product:ATP-binding cassette, sub family B (MDR/TAP), member 1B,
full insert sequence.
ACCESSION AK030328
VERSION AK030328.1 GI:26081769
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
REFERENCE
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE
AUTHORS 2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
AUTHORS 3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Kono,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M.,
Yoneda,Y., Iehikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
AUTHORS 4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE
AUTHORS 5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE
AUTHORS 6 (bases 1 to 3182)
Adachi,J., Aizawa,K., Akimura,T., Aizawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akaike,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toyu,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2001) Yoshinide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail:genome-res@gs.c.riken.jp,
URL:htp://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216]
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:htp://genome.gsc.riken.jp/
URL:htp://fantom.gsc.riken.jp/
FEATURES
source Location/Qualifiers
1..3182
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM:DB:5031438E12"
/db_xref="taxon:10090"
/clone="5031438E12"
/sex="female"
/tissue_type="ovary and uterus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="11 days pregnant adult"

msc_feature 1.3182
/note="ATP-binding cassette, sub-family B (MDR/TRP),
member 1B (MDR1G1:97568, GI:101075, evidence: BLASTN,
99%, match=2587)"

ORIGIN
Query Match 87.2%; Score 21.8; DB 3; Length 3182;
Best Local Similarity 92.0%; Pred. No. 11;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCTA 25
Db 730 AGCTTCCACACCTTATTAATCCTA 706

RESULT 4
LOCUS AY408956/c 3816 bp DNA linear GSS 15-DEC-2003
DEFINITION Mus musculus ABCB1 gene, VIRUTAL TRANSCRIPT, partial sequence,
ACCESSION AY408956
VERSION AY408956.1 GI:39764924
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Cavello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trices
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 3816)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Cavello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
COMMENT
FEATURES
SOURCE Location/Qualifiers
1..3816
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>3816
/gene="ABCB1"
/locus_tag="HMCJ3396"

ORIGIN
Query Match 87.2%; Score 21.8; DB 9; Length 3816;
Best Local Similarity 92.0%; Pred. No. 11;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCTA 25
Db 629 AGCTTCCACACGCGTAATCCTA 605

RESULT 5
LOCUS CF176979/c 682 bp mRNA linear EST 28-JUL-2003
DEFINITION 805414 MARC 3P1G Sue scrofa cDNA 5', mRNA sequence.
ACCESSION CF176979
VERSION CF176979.1 GI:33288755
KEYWORDS EST.
SOURCE Sue scrofa (pig)

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
AUTHORS Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J.,
Wise, T.A., Noneman, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized
library
Unpublished (2003)
JOURNAL Contact: Smith TPL
COMMENT USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_al option. Vector identified with
cross_match v0.990329.
Plate: SRG8002 row: F column: 24
Seq primer: GTAATACGACTCATATAGCG.
Location/Qualifiers

FEATURES
SOURCE 1..682
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_id="MARC 3P1G"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
library made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."

ORIGIN
Query Match 83.2%; Score 20.8; DB 7; Length 682;
Best Local Similarity 91.7%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCTTCCACACGCTGTAATCCT 24
Db 388 AGCTTCCACACCGTAATGCT 365

RESULT 6
LOCUS BE217416/c 478 bp mRNA linear EST 03-JUL-2000
DEFINITION fbn-1094 Cattle pUC18 library Bos taurus cDNA, mRNA sequence.
ACCESSION BE217416
VERSION BE217416.1 GI:8904732
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE
AUTHORS Schweinin, M., Dorroch, U. and Goldammer, T.
TITLE Mapping of differentially expressed hepatic and intestinal EST's in
cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Schwerin M
Molecular Biology
FBN Dummerstorf
2nd Wilhelm-Stahl-Allee, Dummerstorf, 18196, Germany
Tel: 0049-038208-68700
Fax: 0049-038208-68702
Email: schwerin@fbn-dummerstorf.de
High quality sequence stop: 478
POLYA=yes.
Location/Qualifiers

FEATURES
SOURCE 1..478
/organism="Bos taurus"
/mol_type="mRNA"

/db_xref="taxon:9913"
 /sex="female"
 /tissue_type="Intestine"
 /dev_stage="lactation"
 /lab_host="XLI-blue"
 /clone_id="Cattle pUC18 library"
 /note="Vector: pUC18 Sma I/BAD"

ORIGIN

Query Match 80.8%; Score 20.2; DB 2; Length 478;
 Best Local Similarity 80.8%; Pred. No. 54;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGCTTCACACGCTGTAATCCTA 25
 |||||
 Db 309 AGCTTCACACTCTGTAAATCCTA 285

RESULT 7
 CDS0A1M4 806 bp mRNA linear HTC 06-FEB-2004
 LOCUS Arabidopsis thaliana Full-length cDNA complete sequence from clone
 DEFINITION GUSLIT25ZG04 of Siliques of strain col-0 of Arabidopsis thaliana
 (thale cress).
 BX832952
 HX832952.1 GI:42459179
 HTC; GUSL cDNA.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 806)
 Castellani V., Aury J.M., Jallion O., Wincker P., Clepet C.,
 Menard M., Cruaud C., Queciet F., Scarpelli C., Schachter V.,
 Temple G., Caboche M., Weissenbach J. and Salanoubat M.
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
 A Combined Approach to Evaluate and Improve Arabidopsis Genome
 Annotation
 Unpublished
 2 (bases 1 to 806)
 Genoscope.
 Direct Submission
 Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castellani
 V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information Center for Protein
 Sequences) . 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
 Location/Qualifiers
 1. 806
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Col-0"
 /db_xref="taxon:3702"
 /clone="GUSLIT25ZG04"
 /tissue_type="Siliques"
 /plasmid="pCMVSPORT_6"
 1. 806
 /gene="At5g51440"

Best Local Similarity 88.0%; Pred. No. 57;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGCTTCACACGCTGTAATCCTA 25
 |||||
 Db 371 ACCTTCACACGCTGTAATCCTA 347

RESULT 8

AZ957679 489 bp DNA linear GSS 27-APR-2001
 LOCUS 2M0224F07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION clone UUGC2M0224F07 R, genomic survey sequence.
 AZ957679
 A2957679.1 GI:13828906
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 489)
 Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamill C.,
 Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T.,
 Reilly M., Rose M., Rose R., Stokes R., Tingey A., von
 Niederhausern A. and Wright D., Weiss R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0224 row: F column: 07
 Seq primer: CACACGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 489.
 Location/Qualifiers
 1. 489
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0224F07"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castellani
 V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information Center for Protein
 Sequences) . 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
 Location/Qualifiers
 1. 806
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Col-0"
 /db_xref="taxon:3702"
 /clone="GUSLIT25ZG04"
 /tissue_type="Siliques"
 /plasmid="pCMVSPORT_6"
 1. 806
 /gene="At5g51440"

FEATURES

source

gene
 ORIGIN

Query Match 80.8%; Score 20.2; DB 3; Length 806;

TITLE

JOURNAL
 REFERENCE
 AUTHORS

COMMENT
 The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castellani
 V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information Center for Protein
 Sequences) . 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
 Location/Qualifiers
 1. 489
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0224F07"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

ORIGIN

Query Match 79.2%; Score 19.8; DB 8; Length 489;

Best Local Similarity 91.3%; Pred. No. 85;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 AGCTTCACACCGTGAATCC 23
Db 430 AGCTTCACACCGTGAATCC 452

RESULT 9
BI691631 775 bp mRNA linear EST 18-SEP-2001
LOCUS 60330731.F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5343483 5',
DEFINITION mRNA sequence.
ACCESSION BI691631
VERSION BI691631.1 GI:15654260
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE 1 (bases 1 to 775)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC).
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: CGAPdb-rc@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM1872 row: K column: 04
High quality sequence stop: 738.
Location/Qualifiers

FEATURES
source 1..775
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5343483"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_1lb="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
Query Match 79.2%; Score 19.8; DB 4; Length 775;
Best Local Similarity 91.3%; Pred. No. 90;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AGCTTCACACCGTGAATCC 23
Db 604 AGCTTCACACCGTGAATCC 626

RESULT 10
BH521842/c 526 bp DNA linear GSS 13-DEC-2001
LOCUS BH521842
DEFINITION BOGQF60F BOGQ Brassica oleracea genomic clone BOGQF60, genomic
survey sequence.
ACCESSION BH521842
VERSION BH521842.1 GI:17729927
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Town, C.D., Van Aken, S., Uterback, T., Koc, H. and Fraser, C.M.
TITLE 1 (bases 1 to 526)
JOURNAL Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
COMMENT Contact: Chris Town
TRC 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@icigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.
Location/Qualifiers

FEATURES
source 1..526
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGQF60"
/note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN
Query Match 76.8%; Score 19.2; DB 8; Length 526;
Best Local Similarity 87.5%; Pred. No. 176+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AGCTTCACACCGTGAATCC 24
Db 215 ATCTTATACACCGTGAATCCT 192

RESULT 11
AU291400 553 bp mRNA linear EST 04-DEC-2002
LOCUS AU291400 zinnia cultured mesophyll cell equalized cDNA zinnia
DEFINITION elegans cDNA clone Z6035, mRNA sequence.
ACCESSION AU291400
VERSION AU291400.1 GI:24251908
KEYWORDS EST.
SOURCE Zinnia elegans
ORGANISM Zinnia elegans
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Zinnia.
REFERENCE 1 (bases 1 to 553)
AUTHORS Demura, T., Tashiro, G., Horiguchi, G., Kishimoto, N., Kubo, M.,
Matsumoto, N., Minami, A., Nagata-Hiwatashi, M., Nakamura, K.,
Okamura, Y., Sassa, N., Suzuki, S., Yazaki, J., Kikuchi, S. and
Rukuda, H.

TITLE Visualization by comprehensive microarray analysis of gene
expression programs during transdifferentiation of mesophyll cells
into xylem cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
COMMENT Morphogenesis Research Group
RIKEN Plant Science Center
1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9605
Fax: 81-45-503-9573
Email: demura@postman.riken.go.jp
This clone was obtained at our laboratory.
Seq primer: M13 forward
Location/Qualifiers

FEATURES
source 1..553
/organism="Zinnia elegans"
/mol_type="mRNA"
/cultivar="Canary bird"

ORIGIN

Query Match 76.8%; Score 19.2; DB 1; Length 553;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

/db_xref="taxon:34245"
 /clone="Z6035"
 /issue_type="mesophyll cell"
 /clone_lib="Zinnia cultured mesophyll cell equalized cDNA"
 /note="Vector: pGEM-T easy; cultured in tracheary element
 differentiation-inductive medium"

QY 1 AGCTTCACACCGTGAATCCT 24
 |||||
 18 AGCTTCACACCGTGAATCCT 41

RESULT 12

BH174634 589 bp DNA linear GSS 09-OCT-2001
 LOCUS BH174634
 DEFINITION B1r51B20 Mouse IRS-PCR fragment library 57R/b1r Mus musculus
 genomic clone B1r51B20, genomic survey sequence.
 ACCESSION BH174634
 VERSION BH174634.1 GI:15990001
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 589)
 Schalkwyk, L.C., Cusack, B., Dunkel, I., Hopp, M., Kramer, M.,
 Palczewski, S., Pfeffe, J., Scheel, S., Weiher, M., Wenske, G.,
 Lehrach, H. and Himmelbauer, H.
 Advanced integrated mouse YAC map including BAC framework
 Genome Res. 11 (12), 2142-2150 (2001)

TITLE JOURNAL
 MEDLINE 21588072
 PUBMED 11731506

COMMENT Contact: Heinz Himmelbauer
 Department of Vertebrate Genomics/ Abtlg. Lehrach
 Max-Planck-Institute of Molecular Genetics
 Insestr.73, D-14195 Berlin-Dahlem, Germany
 Email: himmelbauer@molgen.mpg.de
 Information on marker localization (Chromosome, map segment) and on
 YACs positive for this probe can be obtained from our web site
 http://www.molgen.mpg.de/(tlide)rodent
 Class: B1-PCR.

FEATURES

Location/Qualifiers

1..589
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="B1r51B20"
 /lab_host="E.coli DH5alpha"
 /clone_lib="Mouse IRS-PCR fragment library 57R/b1r"
 /note="Vector: PAMPI0 (Gibco-BRL); The library was
 generated from IRS-PCR fragments obtained by amplification
 of genomic mouse DNA with the mouse B1-repeat primer B1R
 (5'-AGTTCACACGACGCGCTAACA-3'). Additional
 information online at
 www.molgen.mpg.de/~rodent/html/introduction.html"

ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 589;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGTGAATCCT 24
 |||||
 Db 127 AGCTTCACACCGTGAATCCT 150

RESULT 13

BH713924 604 bp DNA linear GSS 20-FEB-2002
 LOCUS BH713924
 DEFINITION BOMC1387R BO 2.3 KB Brassica oleracea genomic clone BOMC138,
 genomic survey sequence.
 ACCESSION BH713924
 VERSION BH713924.1 GI:18806913
 KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 604)
 Town, C.D., Van Aken, S., Uteirback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 unpublished (2001)
 Other_GSSs: BOMC1387R
 Contact: Chris Town

REFERENCE TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP
 Class: sheared ends.

COMMENT

FEATURES

Location/Qualifiers

1..604
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO100DH3"
 /db_xref="taxon:3712"
 /clone="BOMC138"
 /clone_lib="BO 2.3 KB"
 /note="Vector: pBOS1, Site 1; Bext1; 2-3 kb sheared
 genomic DNA inserted into pBOS1 using Bext1 linkers"

ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 604;
 Best Local Similarity 87.5%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGCTTCACACCGTGAATCCT 24
 |||||
 Db 100 ATCTTATACACGCTGAATCCT 123

RESULT 14

BH696214 617 bp DNA linear GSS 20-FEB-2002
 LOCUS BH696214
 DEFINITION BOMNB047R BO 2.3 KB Brassica oleracea genomic clone BOMNB04,
 genomic survey sequence.
 ACCESSION BH696214
 VERSION BH696214.1 GI:18768830
 KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 617)
 Town, C.D., Van Aken, S., Uteirback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 unpublished (2001)
 Other_GSSs: BOMNB047R
 Contact: Chris Town

REFERENCE TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP

COMMENT

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TP

Class: sheared ends.

FEATURES

Location/Qualifiers

1..617
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOMNB04"
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 /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 617;

Best Local Similarity 87.5%; Pred. No. 1.7e+02; Mismatches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

1 AGCTTCACACCGGTAAATCCT 24
 ||| ||||| ||||| ||||| |||||
 Db 181 ATCTATATACCGGTAAATCCT 204

RESULT 15

BH698731

LOCUS BH698731 634 bp DNA linear GSS 20-FEB-2002

DEFINITION BOMC167TF BO_2_3_KB Brassica oleracea genomic clone BOMC167,
genomic survey sequence.

ACCESSION BH698731

VERSION BH698731.1 GI:18773206

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM

Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 634)
 Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

COMMENT

Location/Qualifiers
 1..634
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 /clone_id="BO_2_3_KB"
 /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"

FEATURES

source

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 /db_xref="taxon:3712"
 /clone="BOMC167"
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 genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 76.8%; Score 19.2; DB 8; Length 634;

Best Local Similarity 87.5%; Pred. No. 1.7e+02; Mismatches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

1 AGCTTCACACCGGTAAATCCT 24
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 Db 65 ATCTATATACCGGTAAATCCT 88

Search completed: February 9, 2005, 21:55:40
 UOB time : 2451.85 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds
(without alignments)
2517.530 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 15
Sequence: 1 gtagacatttcacgacatagcgaa 25

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapex 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmb1:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	AX504310	Sequence
2	25	100.0	25	AX504327	Sequence
3	25	100.0	765	AX706976	Sequence
4	25	100.0	765	AX707906	Sequence
5	25	100.0	765	HUMMDR1A11	Sequence
6	25	100.0	768	AY490254	Sequence
7	25	100.0	3489	AB029153	Sequence
8	25	100.0	3489	AB029153	Sequence
9	25	100.0	3489	AB029153	Sequence
10	25	100.0	3489	AB029153	Sequence
11	25	100.0	3489	AB029153	Sequence
12	25	100.0	3489	AB029153	Sequence
13	25	100.0	3489	AB029153	Sequence
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16	25	100.0	3489	AB029153	Sequence
17	25	100.0	3489	AB029153	Sequence
18	25	100.0	3489	AB029153	Sequence
19	25	100.0	3489	AB029153	Sequence

c	20	25	100.0	4643	6	C0815440	Sequence
c	21	25	100.0	4643	6	AX522070	Sequence
c	22	25	100.0	4643	6	AX587788	Sequence
c	23	25	100.0	4646	6	BD234195	Sequence
c	24	25	100.0	4646	6	C0861565	Sequence
c	25	25	100.0	4646	6	I49610	Sequence
c	26	25	100.0	4646	6	AR380622	Sequence
c	27	25	100.0	4646	6	AX336420	Sequence
c	28	25	100.0	4646	6	AX336708	Sequence
c	29	25	100.0	4646	6	AX331099	Sequence
c	30	25	100.0	4646	6	AX504298	Sequence
c	31	25	100.0	4646	9	HUMMDR1	Sequence
c	32	25	100.0	4646	6	AR055785	Sequence
c	33	25	100.0	4646	6	AR091275	Sequence
c	34	25	100.0	4646	6	I08557	Sequence
c	35	25	100.0	4646	6	AR203322	Sequence
c	36	25	100.0	4646	6	AR363344	Sequence
c	37	25	100.0	4646	6	AR405961	Sequence
c	38	25	100.0	4646	6	AR028671	Sequence
c	39	25	100.0	4646	6	AR306491	Sequence
c	40	25	100.0	4646	6	AR306492	Sequence
c	41	25	100.0	4646	6	AX012320	Sequence
c	42	25	100.0	4646	6	AX012321	Sequence
c	43	25	100.0	4646	6	AR028672	Sequence
c	44	25	100.0	4646	6	AX706975	Sequence
c	45	25	100.0	4646	6	AX707905	Sequence

ALIGNMENTS

RESULT 1	AX504310	Sequence 13 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504310	Sequence 13 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
DEFINITION	AX504310	Sequence 13 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
ACCESSION	AX504310	Sequence 13 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
VERSION	AX504310.1	GI:23386128	25 bp	DNA	linear	PAT 27-SEP-2002
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Db						
RESULT 2	AX504327/c	Sequence 30 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504327	Sequence 30 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
DEFINITION	AX504327	Sequence 30 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
ACCESSION	AX504327	Sequence 30 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
VERSION	AX504327.1	GI:23386139	25 bp	DNA	linear	PAT 27-SEP-2002
KEYWORDS						
SOURCE						
ORGANISM						

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Colgan, S. P.
Compositions and methods for treating hematologic malignancies and multiple drug resistance
Patent: WO 0234291-A 30 02-MAY-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Matches 25; Conservative 0; Mismatches 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
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Db

RESULT 3
AX706976/c
LOCUS AX706976 765 bp DNA linear PAT 04-Apr-2003
DEFINITION Sequence 674 from Patent WO03013534.
ACCESSION AX706976
VERSION AX706976.1 GI:29563301
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Heinrich, G. and Kerb, R.
Methods for the treatment of cancer with irinotecan based on CYP3A5
Patent: WO 03013534-A 674 20-FEB-2003;
Epidaurus Biotechnologie AG (DE)
Location/Qualifiers
1..765
/organism="Homo sapiens"
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ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
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Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
672 GTGACATTTTCACGGCCATAGCGAA 648

Db

RESULT 4
AX707906/c
LOCUS AX707906 765 bp DNA linear PAT 04-Apr-2003
DEFINITION Sequence 674 from Patent WO03013536.
ACCESSION AX707906
VERSION AX707906.1 GI:29563981
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1
Heinrich, G. and Kerb, R.
Methods for treatment of cancer using irinotecan based on UGT1A1
Patent: WO 03013536-A 674 20-FEB-2003;
Epidaurus Biotechnologie AG (DE)
Location/Qualifiers

source 1..765
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ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
672 GTGACATTTTCACGGCCATAGCGAA 648

Db

RESULT 5
HUMMDR1A11/c
LOCUS HUMMDR1A11 765 bp DNA linear PRI 08-JAN-1995
DEFINITION Human P-glycoprotein (MDR1) gene, exons 11, 12 and 13.
ACCESSION M29432 J05168
VERSION M29432.1 GI:187481
KEYWORDS P-glycoprotein; multidrug resistance.
SEGMENT 11 of 26
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source

1 (baees 1 to 765)
Chen, C.-J., Clark, D., Ueda, K., Pastan, I., Gottesman, M.W. and
Roninson, I.B.
Genomic organization of the human multidrug resistance (MDR1) gene
and origin of P-glycoproteins
J. Biol. Chem. 265 (1), 506-514 (1990)
90094448
1967175

Draft entry and computer-readable sequence for [1] kindly submitted
by I.B. Roninson, 27-OCT-1989.

Location/Qualifiers
1..765
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/note="P-glycoprotein; G00-120-712"
127..296
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297..422
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/note="P-glycoprotein"
/number=12
423..535
/gene="PGY1"
/note="PGY1, intron L"
536..739

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exon

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ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 672 GTGACATTTTCACGGCCATAGCGAA 648

RESULT 6
AY490254/c 768 bp DNA linear PRI 27-JAN-2004
LOCUS Homo. sapiens P-glycoprotein (MDR1) gene, partial cds.
DEFINITION
ACCESSION AY490254
VERSION AY490254.1 GI:41058414
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Anitha, A. and Banerjee, M.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-2003) Human Molecular Genetics, Rajiv Gandhi
Centre for Biotechnology, Thiruvananthapuram, Kerala
695014, India

FEATURES

source Location/Qualifiers

1..768
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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KLPH"

ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 768;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 675 GTGACATTTTCACGGCCATAGCGAA 651

RESULT 7
AB029153/c 3489 bp mRNA linear MAM 28-MAR-2002
LOCUS Felis catus multi-drug resistance related mRNA, partial cds.
DEFINITION
ACCESSION AB029153

VERSION AB029153.1 GI:6472652
KEYWORDS Felis catus (cat)
SOURCE Felis catus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE

1
Okai, Y., Nakamura, N., Matsushiro, H., Kato, H., Setoguchi, A.,
Yazawa, M., Okuda, M., Watari, T., Hasegawa, A. and Tsujimoto, H.
Molecular analysis of multidrug resistance in feline lymphoma cells
Am. J. Vet. Res. 61 (9), 1122-1127 (2000)
JOURNAL MEDLINE
PUBMED 10976746
REFERENCE 2 (bases 1 to 3489)
AUTHORS Tsujimoto, H. and Okai, Y.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-1999) Hajime Tsujimoto, The University of Tokyo,
Department of Veterinary Internal Medicine; The University of
Tokyo, Bunkyo-ku, Tokyo 113-8657, Japan
(E-mail:atsuji@hongo.ecc.u-tokyo.ac.jp, Tel: +81-3-5841-8004,
Fax: +81-3-5841-8178)

FEATURES

source Location/Qualifiers

1..3489
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/mol_type="mRNA"
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/cell_type="feline lymphoma cell line"
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KLPH"

ORIGIN

Query Match 100.0%; Score 25; DB 4; Length 3489;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1310 GTGACATTTTCACGGCCATAGCGAA 1286

RESULT 8
AX481416/c 3840 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 30 from Patent WO02055693.
DEFINITION
ACCESSION AX481416
VERSION AX481416.1 GI:22316330
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Haefliger, P.
TITLE Method for inhibiting the expression of a target gene
JOURNAL Patent: WO 02055693-A 30 18-JUL-2002;
Ribopharma AG (DE)

FEATURES
source
1. 3840
/organism="Homo sapiens"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1484 GTGACATTTTCACGGCCATAGCGAA 1460

RESULT 9
BD171402/c
LOCUS BD171402 3843 bp DNA linear PAT 18-FEB-2003
DEFINITION Method for predicting side effects of immunosuppressant and primer
used therefor.
ACCESSION BD171402
VERSION BD171402.1 GI:28412692
KEYWORDS JP 2002223769-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3843)
AUTHORS Ieiri, I.
TITLE Method for predicting side effects of immunosuppressant and primer
used therefor
JOURNAL Patent: JP 2002223769-A 1 13-AUG-2002;
SRL INC

COMMENT OS Homo sapiens (human)
PN JP 2002223769-A/1
PD 13-AUG-2002
PF 31-JAN-2001 JP 2001024723
PI ICHIRO IEIRI
PC C12N15/09, C12N15/68, C12N15/00
CC Method for predicting side effects of immunosuppressant and
CC primer used
CC therefor
FH Key
FT source
FT Location/Qualifiers
1. 3843
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FEATURES
source
1. 3843
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Location/Qualifiers

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 3843;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1487 GTGACATTTTCACGGCCATAGCGAA 1463

RESULT 10
AX322787/c
LOCUS AX322787 3860 bp DNA linear PAT 07-JAN-2002

DEFINITION Sequence 1 from Patent WO0192877.
ACCESSION AX322787
VERSION AX322787.1 GI:18093766
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Sorrentino, B. and Schuetz, J.
TITLE Method of identifying and/or isolating stem cells
JOURNAL Patent: WO 0192877-A 1 06-DEC-2001;
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)

FEATURES
source
1. 3860
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ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 3860;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1487 GTGACATTTTCACGGCCATAGCGAA 1463

RESULT 11
AX322789/c
LOCUS AX322789 3860 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 3 from Patent WO0192877.
ACCESSION AX322789
VERSION AX322789
KEYWORDS AX322789.1 GI:18093767
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Sorrentino, B. and Schuetz, J.
TITLE Method of identifying and/or isolating stem cells
JOURNAL Patent: WO 0192877-A 3 06-DEC-2001;
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)

FEATURES
source
1. 3860
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1487 GTGACATTTTCACGGCCATAGCGAA 1463

RESULT 12
BD190394/c
LOCUS BD190394 3988 bp DNA linear PAT 17-JUL-2003
DEFINITION Phosphatidylcholine as a medicament for the protection of mucosa.
ACCESSION BD190394
VERSION BD190394.1 GI:33000133
KEYWORDS JP 2002522381-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3988)

AUTHORS Stremmel,W.
TITLE Phosphatidylcholine as a medicament for the protection of mucosa
JOURNAL Patent: JP 2002522381-A 1 23-JUL-2002;
Wolfgang STREMMEL
COMMENT OS Homo sapiens
PN JP 2002522381-A/1
PD 23-JUL-2002
PF 06-AUG-1999 JP 2000563262
PR 06-AUG-1998 DE 198 35 526.2,15-DEC-1998 DE 198 57 750.8 PI
Wolfgang stremmel
CC

Query Match 100.0%; Score 25; DB 6; Length 3988;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1553 GTGACATTTTCACGGCCATAGCGAA 1529

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LOCUS AR452556 3988 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6677319.
ACCESSION AR452556
VERSION AR452556.1 GI:42684344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3988)
AUTHORS Stremmel,W.
TITLE Phosphatidylcholine as medication with protective effect large
JOURNAL Intestinal mucosa
Patent: US 6677319-A 1 13-JAN-2004;
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1. .3988
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
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RESULT 14
AX024454/c
LOCUS AX024454 3988 bp DNA linear PAT 15-SEP-2000
DEFINITION Sequence 1 from Patent DE19857750.
ACCESSION AX024454
VERSION AX024454.1 GI:10184622
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
Stremmel,W.
Patent: DE 19857750-A 1 24-FEB-2000;
JOURNAL STREMMEL WOLFGANG (DE)

FEATURES
source Location/Qualifiers
1. .3988
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1553 GTGACATTTTCACGGCCATAGCGAA 1529

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LOCUS AF016535 4192 bp mRNA linear PRI 03-SEP-1997
DEFINITION Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds.
ACCESSION AF016535
VERSION AF016535.1 GI:2353263
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 4192)
AUTHORS Chen,C.J., Chin,J.E., Ueda,K., Clark,D.P., Pastan,I.,
Gottesman,M.M. and Roninson,I.B.
TITLE Internal duplication and homology with bacterial transport proteins
in the mdr1 (P-glycoprotein) gene from multidrug-resistant human
cells
JOURNAL Cell 47 (3), 381-389 (1986)
MEDLINE 87028230
PUBMED 2876781

REFERENCE 2 (bases 1 to 4192)
AUTHORS Chen,G., Duran,G.E., Steger,K.A., Lacayo,N.J., Jaffrezou,J.P.,
Dumontet,C. and Slikic,B.I.
TITLE Multidrug-resistant human sarcoma cells with a mutant
P-glycoprotein, altered phenotype, and resistance to cyclosporins
JOURNAL J. Biol. Chem. 272 (9), 5974-5982 (1997)
MEDLINE 97190336
PUBMED 9038218
REFERENCE 3 (bases 1 to 4192)
AUTHORS Chen,G., Lacayo,N.J., Steger,K.A. and Slikic,B.I.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1997) Medicine, Stanford University School of
Medicine, Stanford, CA 94306, USA
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source Location/Qualifiers
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FEHMYAQSLOVPYNSLRKAHIFGITSFTQAMMYFSYACGFRGAYLVAKHLMSEED
VLIVFSAVVFAGAAVGOVSSFPAPYAKAKISAHIIWIEKTPIDISYSEGMPNTL
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659

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ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 4192;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
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Db 1603 GTGACATTTTCACGGCCATAGCGAA 1579

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Job time : 482.178 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 78.592 Seconds
(without alignments)
520.498 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	25	100.0	4284	2	US-08-784-649A-1
C 3	25	100.0	4264	2	US-08-784-649A-5
C 4	25	100.0	4646	1	US-08-181-471-2
C 5	25	100.0	4646	2	US-09-023-655-1167
C 6	25	100.0	4669	2	US-08-583-276-18
C 7	25	100.0	4669	2	US-08-752-447-1
C 8	25	100.0	4669	3	US-09-316-167-1
C 9	25	100.0	4669	4	US-09-397-233-1
C 10	25	100.0	4669	6	5206352-3
C 11	25	100.0	4669	6	5206352-3
C 12	25	100.0	8630	2	US-08-793-610-5
C 13	25	100.0	8630	4	US-09-306-417-2
C 14	25	100.0	8630	4	US-09-306-417-2
C 15	25	100.0	9318	2	US-08-793-610-6
C 16	25	100.0	9318	4	US-09-672-725C-1
C 17	25	100.0	9318	4	US-09-672-725C-1
C 18	25	100.0	9318	4	US-09-672-725C-22
C 19	25	100.0	9318	4	US-09-672-725C-22
C 20	25	100.0	9318	4	US-09-672-725C-26
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C 22	25	100.0	9318	4	US-09-672-725C-26
C 23	25	100.0	9318	4	US-09-672-725C-26
C 24	25	100.0	9318	4	US-09-672-725C-26
C 25	25	100.0	9318	4	US-09-672-725C-26
C 26	25	100.0	9318	4	US-09-672-725C-26
C 27	25	100.0	9318	4	US-09-672-725C-26

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C 29	21.8	87.2	4233	4	US-09-450-105-1	Sequence 1, Appli
C 30	19	76.0	3321	4	US-09-640-173-175	Sequence 175, App
C 31	19	76.0	3321	4	US-09-713-550-175	Sequence 175, App
C 32	19	76.0	3321	4	US-09-825-294-175	Sequence 175, App
C 33	19	76.0	3321	4	US-09-970-966-175	Sequence 175, App
C 34	18.6	74.4	3924	4	US-09-023-655-1168	Sequence 1,68, Ap
C 35	18.6	74.4	3924	4	US-09-762-195-2	Sequence 2, Appli
C 36	18.2	72.8	601	4	US-09-949-016-61079	Sequence 61079, A
C 37	18.2	72.8	723	4	US-09-016-434-1422	Sequence 1422, Ap
C 38	18.2	72.8	1255	4	US-09-949-016-1772	Sequence 1772, Ap
C 39	18.2	72.8	1446	3	US-08-787-091-1	Sequence 1, Appli
C 40	18.2	72.8	8137	4	US-09-566-921-7	Sequence 7, Appli
C 41	18.2	72.8	47698	4	US-09-949-016-13514	Sequence 13514, A
C 42	17.8	71.2	26	1	US-08-227-370-4	Sequence 4, Appli
C 43	17.8	71.2	26	5	PCT-US94-06284-4	Sequence 186, App
C 44	17.6	70.4	945	4	US-09-134-000C-186	Sequence 11434, A
C 45	17.4	69.6	616	4	US-09-270-767-11434	

ALIGNMENTS

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RESULT 1
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; Sequence 1, Application US/09762195
; Patent No. 6677319
; GENERAL INFORMATION:
; APPLICANT: Streemmel, Wolfgang
; TITLE OF INVENTION: Phosphatidylcholine as Medication with
; TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
; FILE REFERENCE: 34691/208520
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: PCT/EP9702426
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 198 35 526 2 DE
; PRIOR FILING DATE: 1998-08-06
; PRIOR APPLICATION NUMBER: 198 57 570.8 DE
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-1
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Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1553 GTGACATTTTCACGCCCATAGCGAA 1529
RESULT 2
US-08-784-649A-1/c
; Sequence 1, Application US/08784649A
; Patent No. 5830697
; GENERAL INFORMATION:
; APPLICANT: Shtic, Branimir I
; TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
; TITLE OF INVENTION: CYCLOSPORIN MODULATION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
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ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-784-649A-1

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Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1625 GTGACATTTTCACGGCCATAGCGAA 1601

RESULT 3
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Sequence 5, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: Sixic, Branimir I
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-784-649A-5

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Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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Sequence 2, Application US/08181471
Patent No. 5641508
GENERAL INFORMATION:
APPLICANT: Li, Lingna
APPLICANT: Liebko, Valeryi K.
TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas Fitting
STREET: 12526 High Bluff Drive, Suite 300
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92130
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,471
FILING DATE: 13-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,553
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: ANT0029P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-792-3680
TELEFAX: 619-792-8477
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4267
US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 5

US-09-023-655-1167/c
 ; Sequence 1167, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooke, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
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 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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 ; FILING DATE: HEREMITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1167:
 ; SEQUENCE CHARACTERISTICS:
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 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
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 ; CLONE: 9187468
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 DB 1911 GTGACATTTTCACGGCCCATAGCGAA 1887
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 RESULT 6
 US-08-583-276-18/c
 ; Sequence 18, Application US/08583276
 ; Patent No. 5837536
 ; GENERAL INFORMATION:
 ; APPLICANT: McDonagh, Kevin T.
 ; APPLICANT: Nienhuis, Arthur
 ; APPLICANT: Tolstoshev, Paul
 ; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
 ; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
 ; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carella, Byrne, Bain, Giffillan,
 ; ADDRESSEE: Cecchi & Stewart
 ; STREET: 6 Becker Farm Road

CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
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 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: DM4 V2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/583,276
 ; FILING DATE: 05-JAN-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/332,444
 ; FILING DATE: 31-OCT-1994
 ; APPLICATION NUMBER: 07/887,712
 ; FILING DATE: 22-MAY-1992
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4669 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: singular
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; DESCRIPTION: Genomic DNA
 ; US-08-583-276-18
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 Query Match 100.0%; Score 25; DB 2; Length 4669;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 GTGACATTTTCACGGCCCATAGCGAA 25
 ;
 DB 1911 GTGACATTTTCACGGCCCATAGCGAA 1887
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 RESULT 7
 US-08-752-447-1/c
 ; Sequence 1, Application US/08752447
 ; Patent No. 5994088
 ; GENERAL INFORMATION:
 ; APPLICANT: Mechtner, Eugene
 ; APPLICANT: Robinson, Igor B
 ; TITLE OF INVENTION: Methods and Reagents for Preparing and
 ; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
 ; STREET: 300 South Wacker Drive, Seventh Floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/752,447
 ; FILING DATE: 15-NOV-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5994088nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 95,1121
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-913-9808
 ; TELEFAX: 312-913-0001
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4669 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-08-752-447-1

Query Match 100.0%; Score 25; DB 2; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGCGCATAGCGAA 25
DB 1911 GTGACATTTTCACGCGCATAGCGAA 1887

RESULT 8

US-09-316-167-1/c
Sequence 1, Application US/09316167

Patent No. 6365357

GENERAL INFORMATION:

APPLICANT: Mechetter, Eugene

APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Methods and Reagents for Preparing and

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: McDonnell Boehnen Hulbert & Berghoff Ltd.

STREET: 300 South Wacker Drive, Seventh Floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/316.167

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/752.447

FILING DATE: 15-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: No. 6365357nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 95,1121

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001

TELEFAX: 312-913-9808

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4669 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..424

FEATURE:

NAME/KEY: CDS

LOCATION: 425..4264

FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-09-316-167-1

Query Match 100.0%; Score 25; DB 3; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGCGCATAGCGAA 25
DB 1911 GTGACATTTTCACGCGCATAGCGAA 1887

RESULT 9

US-09-397-233-1/c
Sequence 1, Application US/09397233

Patent No. 6630327

GENERAL INFORMATION:

APPLICANT: Mechetter, Eugene

APPLICANT: Roninson, Igor B

TITLE OF INVENTION: Methods and Reagents for Preparing and

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: McDonnell Boehnen Hulbert & Berghoff

STREET: 300 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/397,233

FILING DATE: 16-Sep-1999

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: No. 6630327nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 95,1121-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4669 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..424

FEATURE:

NAME/KEY: CDS

LOCATION: 425..4264

FEATURE:

NAME/KEY: 3'UTR

LOCATION: 4265..4669

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 100.0%; Score 25; DB 4; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGCGCATAGCGAA 25
DB 1911 GTGACATTTTCACGCGCATAGCGAA 1887

RESULT 10
5206352-3/c
Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO:3:
LENGTH: 4669
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 11
5206352-3/c
Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO:3:
LENGTH: 4669
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 12
US-08-793-610-5/c
Sequence 5, Application US/08793610
Patent No. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARBERS, Carol
APPLICANT: OSTERING, Wolfgang
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP

STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-793-610-5

Query Match 100.0%; Score 25; DB 2; Length 6505;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 3303 GTGACATTTTCACGGCCATAGCGAA 3279

RESULT 13
US-09-306-417-1/c
Sequence 1, Application US/09306417
Patent No. 6548301
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral
OTHER INFORMATION: plasmid DNA
NAME/KEY: misc.feature
LOCATION: (1)..(160)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:

```
NAME/KEY: misc.feature
LOCATION: (161)..(677)
OTHER INFORMATION: 5'-LTR
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (532)..(1219)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: (1220)..(5062)
OTHER INFORMATION: m4 mdr-1 CDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5215)..(5774)
OTHER INFORMATION: 3'-LTR
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SPdelta71m4
US-09-306-417-1
```

```
Query Match 100.0%; Score 25; DB 4; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTGACATTTTCACGCCCATAGCGAA 25
DB 2706 GTGACATTTTCACGCCCATAGCGAA 2682
```

```
RESULT 14
US-09-306-417-2/c
Sequence 2, Application US/09306417
Patent No. 6548301
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral
OTHER INFORMATION: plasmid DNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SPdelta91MSAI
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(160)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (161)..(677)
OTHER INFORMATION: 5'-LTR
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (532)..(1219)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: (1220)..(5062)
OTHER INFORMATION: msa1 mdr1 CDNA
```

```
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5215)..(5774)
OTHER INFORMATION: 3'-LTR
FEATURE:
NAME/KEY: misc.feature
LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid backbone (pUC)
US-09-306-417-2
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Query Match 100.0%; Score 25; DB 4; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTGACATTTTCACGCCCATAGCGAA 25
DB 2706 GTGACATTTTCACGCCCATAGCGAA 2682
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RESULT 15
US-08-793-610-6/c
Sequence 6, Application US/08793610
Patent No. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARRIS, Carol
APPLICANT: OSTERAG, Wolfram
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaide, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-08-793-610-6
```

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Query Match 100.0%; Score 25; DB 2; Length 9318;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 GTGACATTTTCACGGCCATAGCGAA 25
|||
Db 3262 GTGACATTTTCACGGCCATAGCGAA 3238
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Search completed: February 9, 2005, 17:11:18
Job time : 79.592 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds
(without alignments)
602.360 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 1 gtegacatttcacgscacatagcgaa 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_16Dec04.*

1: geneseq19808.*
2: geneseq19908.*
3: geneseq20008.*
4: geneseq20018.*
5: geneseq20028.*
6: geneseq20038.*
7: geneseq20048.*
8: geneseq20058.*
9: geneseq20068.*
10: geneseq20078.*
11: geneseq20088.*
12: geneseq20098.*
13: geneseq20108.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AAD39002 Human mdr
2	25	100.0	25	6	AAD39012 Human mdr
3	25	100.0	219	12	ACH82796 Human gen
4	25	100.0	584	12	ACH69096 Human gen
5	25	100.0	765	3	AAA96071 Human Pgp
6	25	100.0	765	8	ACF62746 Cancer ba
7	25	100.0	765	8	ADB20861 MRPL base
8	25	100.0	765	10	ADB87950 Human UGT
9	25	100.0	765	10	ADB96933 Human MDR
10	25	100.0	765	10	ADB92124 Human MDR
11	25	100.0	2307	6	AB865230 CDNA enco
12	25	100.0	3840	6	ABV78146 Human mdr
13	25	100.0	3840	6	ABZ35722 Human mdr
14	25	100.0	3840	6	ABX09965 Human mdr
15	25	100.0	3840	6	ABY19167 Human pol
16	25	100.0	3843	6	ABQ78185 Human MDR
17	25	100.0	3860	3	AAZ49332 Human w11
18	25	100.0	3860	3	AAZ49333 Human G18
19	25	100.0	3860	6	ABA94365 Human BCR
20	25	100.0	3860	6	ABA94366 Human BCR

C 21	25	100.0	3988	3	AAZ88973 Human MDR
C 22	25	100.0	4264	2	AAV65533 Mutated h
C 23	25	100.0	4264	2	AAV65534 Mutated h
C 24	25	100.0	4349	4	AAH57442 Human int
C 25	25	100.0	4378	2	AAQ04522 Multidrug
C 26	25	100.0	4533	6	AB855229 CDNA enco
C 27	25	100.0	4533	6	AB855229 CDNA enco
C 28	25	100.0	4643	6	ABV94267 Breast ca
C 29	25	100.0	4643	6	ABV94267 Breast ca
C 30	25	100.0	4643	6	ABV77217 CDNA enco
C 31	25	100.0	4643	12	ABX77217 CDNA enco
C 32	25	100.0	4643	12	ADP18689 Human PRO
C 33	25	100.0	4643	13	ADP54881 Human PRO
C 34	25	100.0	4646	2	AAQ72872 Human mul
C 35	25	100.0	4646	3	AAZ94738 Human ATP
C 36	25	100.0	4646	6	ABL68592 Kidney ca
C 37	25	100.0	4646	6	ABL68592 Kidney ca
C 38	25	100.0	4646	6	ABL68880 Kidney ca
C 39	25	100.0	4646	10	ADK60994 Human mdr
C 40	25	100.0	4646	11	ADK60994 Ovarian C
C 41	25	100.0	4646	11	ADJ31841 Human CDN
C 42	25	100.0	4649	1	ADR52847 Drug ther
C 43	25	100.0	4649	2	AAQ52726 Sequence
C 44	25	100.0	4649	2	AAV32645 Human P g
C 45	25	100.0	4669	6	ABK52041 CDNA enco

ALIGNMENTS

RESULT 1	AAD39002	standard; DNA, 25 BP.
ID	AAD39002	standard; DNA, 25 BP.
XX	AC	AAD39002;
XX	AC	23-SEP-2002 (first entry)
XX	DE	Human mdr1-HRE antisense oligonucleotide #5.
XX	XX	Human; hematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoma; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythemia; myeloma; angioendothelial myeloid metaplasia; myeloid leukaemia; gene therapy; polycythemia vera; hypoxia responsive element; HRE; antisense; phosphorothioate backbone; ss.
XX	KW	Homo sapiens.
XX	OS	Synthetic.
XX	FX	Key
XX	FX	modified_base
XX	FT	Location/Qualifiers
XX	FT	1..25
XX	FT	/*tag= a
XX	FT	/mod_base= OTHER
XX	FT	/note= "phosphorothioate backbone"
XX	XX	W0200234291-A2.
XX	XX	02-MAY-2002.
XX	XX	25-OCT-2001; 2001WO-US049856.
XX	XX	26-OCT-2000; 2000US-0243542P.
XX	XX	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX	XX	Colgan SP;
XX	XX	WPI; 2002-471427/50.
XX	XX	Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
PT binding molecules.
PS Claim 14; Page 43; 92pp; English.
XX
XX The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is an antisense
CC oligo targeted to HRE in the mdrl gene (mdrl-HRE) to inhibit its
CC expression. This oligo is used in the exemplification of the invention
XX
SQ Sequence 25 BP; 7 A; 6 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1 GTGACATTTTCACGGCCATAGCGAA 25
RESULT 2
AAD39012/c
ID AAD39012 standard; DNA; 25 BP.
XX
AC AAD39012;
XX
XX 23-SEP-2002 (first entry)
XX
XX Human mdrl gene HIF-1 binding site DNA #5.
XX
XX Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;
XX hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;
XX lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
XX myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;
XX angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;
XX polycythaemia vera; hypoxia responsive element; HRE; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_binding 11..15
FT /*cage= a
FT /bound_molety= "HIF-1"
XX
XX WO200234291-A2.
XX
XX 02-MAY-2002.
XX
XX 25-OCT-2001; 2001WO-US049856.
XX
XX 26-OCT-2000; 2000US-0243542P.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
XX Colgan SP;
XX
XX WPI; 2002-471427/50.
XX
XX Treating a subject (at risk of) having a hematologic malignancy or
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
PT binding molecules.
PS Example 2; Page 12; 92pp; English.
XX
XX The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angiotenic
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is human mdrl
CC gene HIF-1 binding site DNA
XX
SQ Sequence 25 BP; 6 A; 6 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 25 GTGACATTTTCACGGCCATAGCGAA 1
RESULT 3
ACH82796
ID ACH82796 standard; DNA; 219 BP.
XX
XX ACH82796;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon probe #15991.
XX
XX Human genome derived single exon probe; microarray;
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX OS US2003194704-A1.
XX
XX PN 16-OCT-2003.
XX
XX PD 03-APR-2002; 2002US-00029386.
XX
XX PF 03-APR-2002; 2002US-00029386.
XX
XX PR 03-APR-2002; 2002US-00029386.
XX
XX PA (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
XX
XX DR New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX gene expression events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
XX PS Claim 1; SEQ ID NO 15991; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and

Query Match	Best Local Similarity	Score 25;	DB 12;	Length 219;
Matches 25;	Conservative 0;	Mismatches	Indels 0;	Gaps 0
Qy	1 GTGACATTTTCACGGCCATAGCGGAA 25			
Db	77 GTGACATTTTCACGGCCATAGCGGAA 101			
<p>RESULT 4</p> <p>ACH69096</p> <p>ID ACH69096 standard; DNA; 584 BP.</p> <p>XX ACH69096;</p> <p>XX</p> <p>DT 29-JUL-2004 (first entry)</p> <p>XX</p> <p>DE Human genome derived single exon probe #2291.</p> <p>XX</p> <p>XX Human; probe; ss; gene expression; single exon probe; microarray;</p> <p>KW alternative splicing event; genomic alteration.</p> <p>XX</p> <p>OS Homo sapiens.</p> <p>PN US2003194704-A1.</p> <p>PD 16-OCT-2003.</p> <p>PF 03-APR-2002; 2002US-00029386.</p> <p>PR 03-APR-2002; 2002US-00029386.</p> <p>XX</p> <p>XX (PENN/) PENN S G.</p> <p>PA (RANK/) RANK D R.</p> <p>PA (HANZ/) HANZEL D K.</p> <p>XX</p> <p>XX Penn SG, Rank DR, Hanzel DK;</p> <p>XX</p>				

XX WPI; 2004-119264/12.

PT New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX Claim 15; SEQ ID NO 2291; 80pp; English.

PS The invention relates to a nucleic acid probe for measuring human gene

XX expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridises under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above-mentioned amino acid

CC sequences (optionally with conservative amino acid substitutions), a

CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to

CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable

CC storage medium which contains a database having a plurality of records

CC (each record including data on the expression of a single exon probe

CC cited above. The probe, methods and apparatus are useful in gene

CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their

CC specific exon, or in constructing genome-derived single exon microarrays.

CC In addition, the probes are used in identifying and characterising

CC alternative splicing events, in detecting and characterising gross

CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,

CC or in expressing the ORF-encoded peptide. The present sequence is a human

CC single exon probe of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from USPTO at

CC segdata.uspto.gov/sequence.html?docID=20030194704

XX
XX
SQ Sequence 584 BP; 166 A; 139 C; 100 G; 179 T; 0 U; 0 Other;

QY
DB

Query Match 100.0%; Score 25; DB 12; Length 584;
Best Local Similarity 100.0%; Pred.No. 0.024;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 GTGACATTTTCAGCGCCATTAGCGAA 25
|||||
320 GTGACATTTTCAGCGCCATTAGCGAA 344

RESULT 5
AAA96071/c
ID AAA96071 standard; DNA; 765 BP.
XX
XX AAA96071;
DT
XX
XX 29-JAN-2001 (first entry)
DE Human Pgp ATP binding cassette (ABC) transporter coding sequence.
XX
XX Drug resistance; ATP gradient; chemotherapeutic; antibiotic; herbicide;
KW human; ATP binding cassette; ABC transporter; ds.
XX
XX Homo sapiens.
OS
XX
PN WO200052144-A1.
XX

PD 08-SEP-2000.
XX
PF 28-FEB-2000; 2000WO-US005315.
XX
PR 03-MAR-1999; 99US-00261825.
XX
PA (TEXA) UNIV TEXAS.
XX
PI Thomas CE, Windsor JB, Roux SJ, Lloyd AM, Hurley L;
XX WPI; 2000-587306/55.
DR
XX Increasing or decreasing drug resistance in target bacteria, yeast, plant
PT or mammalian cells comprises altering ATP gradient across biological
PT membrane of target cell.
XX
PS Claim 15; Page; 85pp; English.
XX
CC The present invention relates to a method for increasing or decreasing
CC drug resistance in target bacteria, yeast, plant or mammalian cells by
CC altering the ATP gradient across the biological membrane of the target
CC cell. The method is useful for modulating drug resistance of cells. It is
CC useful for increasing the sensitivity of cells to chemotherapeutic and
CC antibiotic agents and increasing resistance to herbicides. The present
CC sequence is human Pgp ATP binding cassette (ABC) transporter coding
CC sequence. This sequence was used in the present invention to modulate
CC drug resistance. Note: The present sequence is not shown in the
CC specification, but is referred to via its Genbank accession number
XX
SQ Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 672 GTGACATTTTCACGGCCATAGCGAA 648

RESULT 6
ACF62746/c
ID ACF62746 standard; DNA; 765 BP.
XX
AC ACF62746;
XX
DT 08-OCT-2003 (first entry)
XX
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:674.
XX
KM Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
KM cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
KM cytochrome; gene; de.
XX
OS Unidentified.
XX
PN WO2003013534-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008219.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX WPI; 2003-268144/26.
DR
XX New use of irinotecan for preparation of compositions for treating cancer
PT in subject having genome with variant allele comprising cytochrome p450,

PT subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
XX
XX Disclosure; SEQ ID NO 674; 86pp; English.
XX
CC The present invention describes the use of irinotecan (I) or its
CC derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic
CC cancer, or malignant glioma in a subject having a genome with a variant
CC allele which comprises a cytochrome p450, subfamily IIIA (nifedipine
CC oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have
CC cytostatic activity. The therapeutic applications of (I) is improved,
CC since it is possible to individually treat a subject with an appropriate
CC dosage and/or an appropriate derivative of (I). Therefore, undesirable,
CC harmful or toxic effects are efficiently avoided. Unnecessary and
CC potentially harmful treatment of those subjects who do not respond to the
CC treatment with substances (nonresponders), as well as the development of
CC drug resistances due to suboptimal drug dosing can be avoided. ACF62200
CC to ACF62751 and ABM34912 to ABM35013 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 765;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 672 GTGACATTTTCACGGCCATAGCGAA 648

RESULT 7
ADB20861/c
ID ADB20861 standard; DNA; 765 BP.
XX
AC ADB20861;
XX
DT 20-NOV-2003 (first entry)
XX
DE MRP1 based cancer related nucleic acid SEQ ID NO:674.
XX
KM irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KM lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
KM de.
XX
OS Unidentified.
XX
PN WO2003013533-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-EP008200.
XX
PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Heinrich G, Kerb R;
XX WPI; 2003-354397/33.
DR
XX Use of irinotecan or its derivative for preparation of a pharmaceutical
PT composition for treating cancer in a subject having a genome with a
PT variant allele comprising a multidrug resistance protein 1
PT polynucleotide.
XX
PS Disclosure; SEQ ID NO 674; 100pp; English.
XX
CC The present invention describes a method for the use of irinotecan (I) or
CC its derivative for the preparation of a pharmaceutical composition for
CC treating colorectal, cervical, gastric, lung, ovarian or pancreatic

Query Match		100.0%;	Score 25;	DB 10;	Length 765;
Best Local Similarity		100.0%;	Pred. No. 0.026;		
Matches	25;	Conservative	0;	Mismatches	0;
				Indels	0;
Gy	1 GTGACATTTTCACGGCCATTAGCGAA 25 				
Db	672 GTGACATTTTCACGGCCATTAGCGAA 648				

RESULT 9

ID	ADB96933/c
XX	ADB96933 standard; DNA; 765 BP.
AC	ADB96933;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Human MDR1 related DNA sequence SEQ ID NO:674.
KX	irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW	lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KM	multidrug resistance 1; MDR1; cytostatic; human; CYP3A5; MKP1; MDR1;
KM	TOP1; ds.
XX	
OS	Homo sapiens.
PN	MO2003013537-A2.
PD	20-FEB-2003.
PF	23-JUL-2002; 2002WO-EP008218.
PR	23-JUL-2001; 2001EP-00117608.
PR	24-MAY-2002; 2002EP-00011710.
PA	(EPID-) EPIDAUKROS BIOTECHNOLOGIE AG.
PI	Heinrich G, Korb R;
DR	WPI; 2003-268145/26.
PT	New use of irinotecan for preparation of pharmaceutical compositions for treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
PS	Disclosure; SEQ ID NO 674; 130pp; English.
XX	The invention relates to the novel use of irinotecan or its derivative for the preparation of pharmaceutical compositions for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition of the invention has cytostatic activity. The invention is useful for the preparation of pharmaceutical compositions for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject (preferably human, more preferably African or Asian) or a mouse. The present sequence is used in the exemplification of the invention.
SQ	Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;

Query Match		100.0%;	Score 25;	DB 10;	Length 765;
Best Local Similarity		100.0%;	Pred. No. 0.026;		
Matches	25;	Conservative	0;	Mismatches	0;
				Indels	0;
Gy	1 GTGACATTTTCACGGCCATTAGCGAA 25 				
Db	672 GTGACATTTTCACGGCCATTAGCGAA 648				

RESULT 10

ID	ADB92124/c
AD	ADB92124 standard; DNA; 765 BP.

```

XX AC ADB92124;
XX DT 04-DEC-2003 (first entry)
XX DE Human MDR1 related DNA sequence SEQ ID NO:674.
XX KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;
XX KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
XX KW multidrug resistance 1; MDR1; cytosolic; human; UGT1A1; MRP1; TOP1; ds.
XX OS Homo sapiens.
XX PN MO2003013535-A2.
XX PD 20-FEB-2003.
XX PF 23-JUL-2002; 2002MO-EP008220.
XX PR 23-JUL-2001; 2001EP-00117608.
XX PR 24-MAY-2002; 2002EP-00011710.
XX PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX PI Heinrich G, Kerb R;
XX DR WPI; 2003-342400/32.
XX PT New use of irinotecan for preparation of pharmaceutical compositions for
XX PT treating cancer in subject having genome with variant allele comprising
XX PT multidrug resistance 1 polynucleotide.
XX PS Disclosure; SEQ ID NO 674; 104bp; English.
XX CC The invention relates to a novel use of irinotecan or its derivative for
XX CC the preparation of a pharmaceutical composition for treating colorectal,
XX CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
XX CC glioma in a subject having a genome with a variant allele which comprises
XX CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
XX CC invention has cytostatic activity. The present sequence is used in the
XX CC exemplification of the invention.
XX CC
XX CC Sequence 765 BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;
SQ
XX Query Match 100.0%; Score 25; DB 10; Length 765;
XX Best Local Similarity 100.0%; Pred. No. 0.026;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACATTTTCACGCGCATAGCGAA 25
DB 672 GTGACATTTTCACGCGCATAGCGAA 648

RESULT 11
AB565230/C
ID AB565230 standard; cDNA; 2307 BP.
XX
XX AC AB565230;
XX DT 15-NOV-2002 (first entry)
XX DE cDNA encoding tumour involved gene (TIG) splice variant, NV-31.
XX KW Human; 6s; gene; splice variant; tumour-involved gene; TIG;
XX KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
XX KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
XX KW gene therapy.
XX OS Homo sapiens.
XX PN US2002086384-A1.
XX PD 04-JUL-2002.

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XX PF 13-MAR-2001; 2001US-00805020.
XX PR 14-MAR-2000; 2000IL-00135402.
XX PR 16-MAY-2000; 2000IL-00136154.
XX PA (LEVI/) LEVINE Z.
XX PA (DAVI/) DAVID A.
XX PA (ROMA/) ROMANO C.
XX PA (BERN/) BERNSTEIN J.
XX PI Levine Z, David A, Romano C, Bernstein J;
XX PN WPI; 2002-635679/68.
XX DR P-PSDB; ABG79700.
XX PT Novel nucleic acid sequence, which is an alternative splicing variant of
XX PT tumor involved genes, useful for detecting cancer, predisposition to
XX PT cancer, for evaluating cancer state and in gene therapy for treating
XX PT cancer.
XX PS Claim 1; Page 60-61; 180bp; English.
XX CC The invention discloses isolated human nucleic acid alternative splicing
XX CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
XX CC polypeptides are useful for determining the level of a nucleic acid or
XX CC polypeptide in a biological sample, for detecting a variant nucleic acid
XX CC or polypeptide sequence in a biological sample, for determining the level
XX CC of variant nucleic acid or polypeptide sequences in a biological sample
XX CC and for determining the ratio between the level of variant sequence in a
XX CC first biological sample and the level of the original sequence from which
XX CC the variant has been varied by alternative splicing in a second
XX CC biological sample and for raising antibodies. A pharmaceutical
XX CC composition comprising a carrier and the nucleic acid, is useful for
XX CC treating diseases (e.g. cancer) that can be ameliorated or cured by
XX CC increasing or decreasing the level of the encoded protein. The nucleic
XX CC acids are also useful for diagnostic purposes, especially for detecting
XX CC cancer or a predisposition to cancer, for evaluating the state or
XX CC aggressiveness of cancer disease, in basic research, for understanding
XX CC the physiological function of the original TIG, in targeting or
XX CC developing pharmaceuticals, for distinguishing various stages in the life
XX CC cycle of the same type of cells which may be helpful for the development
XX CC of pharmaceuticals for various cancer stages in which cell cycle is non-
XX CC normal, for determining mutations in tumour-involved genes and in gene
XX CC therapy. The polypeptides are useful for identifying compounds capable of
XX CC binding to the variant product and modulating its activity and for
XX CC modulating endothelial differentiation and proliferation, as well as to
XX CC modulate apoptosis either ex vivo or in vivo. The sequences presented in
XX CC AB5652200-AB565235 are the coding sequences for the new variants (NV) 1-
XX CC 36 of the TIGs disclosed
XX CC
XX CC Sequence 2307 BP; 662 A; 441 C; 591 G; 612 T; 0 U; 1 Other;
SQ
XX Query Match 100.0%; Score 25; DB 6; Length 2307;
XX Best Local Similarity 100.0%; Pred. No. 0.032;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACATTTTCACGCGCATAGCGAA 25
DB 1911 GTGACATTTTCACGCGCATAGCGAA 1887

RESULT 12
ABV78146/C
ID ABV78146 standard; DNA; 3840 BP.
XX
XX AC ABV78146;
XX DT 15-NOV-2002 (first entry)
XX DE Human mdr-1 DNA SEQ ID NO 30.
XX KW RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytosolic;

```



```

PR 09-JAN-2001; 2001DE-01000588.
XX (RIBO-) RIBOPHARMA AG.
XX PA
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX DR
XX WPI; 2002-683450/74.
XX PR
XX Inhibiting expression of target genes, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.
XX PS
XX Claim 13; Page 27-28; 100pp; German.
XX
XX The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligoribonucleotides (dsRNA and II'), both
CC CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNA and II' are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumors
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, degradability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
XX
XX
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1484 GTGACATTTTCACGGCCATAGCGAA 1460
RESULT 14
ABX09965/C
ID ABX09965 standard; DNA; 3840 BP.
XX
XX ABX09965;
XX
XX 23-JAN-2003 (first entry)
XX DT
XX Human mdr-1 DNA fragment SEQ ID 30.
XX DE
XX Oligoribonucleotide; interferon; oncogene; cytokine; id; developmental;
XX KW
XX prion; inhibition; human; ds.
XX XX
XX Homo sapiens.
XX OS
XX DE10100587-C1.
XX PN
XX 21-NOV-2002.
XX PD
XX 09-JAN-2001; 2001DE-01000587.
XX PF
XX 09-JAN-2001; 2001DE-01000587.
XX PR
XX (RIBO-) RIBOPHARMA AG.
XX PA
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX PI
XX WPI; 2002-742209/81.
XX DR
XX Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT introduction of complementary double-stranded oligoribonucleotide, after
PT treating the cell with interferon.
PT

```

XX Disclosure; Page 32-33; 98pp; German.
 XX
 PS
 CC This invention describes a novel method for inhibiting expression of a
 CC target gene by introducing into the cell that contains the target gene at
 CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
 CC structure of not more than 49 consecutive nucleotides (nt), where at
 CC least a segment of one strand of the ds structure is complementary with
 CC the target gene and the cells are treated with interferon before
 CC introduction of dsRNA. The method is used to inhibit expression of
 CC target genes, particularly oncogenes, cytokine genes, id (not defined)
 CC protein genes; developmental or prion genes, or genes expressed in
 CC pathogenic organisms (particularly plasmodia) or in viruses or viroids
 CC (pathogenic in humans, animals or plants). Treating the cells with
 CC interferon greatly increases the extent to which dsRNA can inhibit
 CC expression of the target genes, and the effect is even greater when dsRNA
 CC are modified to increase their stability. ABX0936-ABX10075 represent
 CC gene fragments used to illustrate the method of the invention
 XX
 SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 6; Length 3840;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GTGACATTTTCACGGCCATAGCGAA 25
 DB 1484 GTGACATTTTCACGGCCATAGCGAA 1460
 RESULT 15
 ABL91687/C
 ID ABL91687 standard; DNA; 3840 BP.
 AC ABL91687;
 XX
 DT 28-MAY-2002 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 30.
 XX
 KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
 KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
 KW cytosatic; virucide; protozoacide; antibacterial; ds.
 XX
 OS Homo sapiens.
 XX
 PN DE10100586-C1.
 XX
 PD 11-APR-2002.
 XX
 PF 09-JAN-2001; 2001DE-01000586.
 XX
 PR 09-JAN-2001; 2001DE-01000586.
 XX
 PA (RIBO-) RIBOPHARMA AG.
 XX
 PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
 XX
 DR WPI; 2002-270454/32.
 XX
 PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by
 PT introducing double-stranded complementary oligoRNA having unpaired
 PT terminal bases.
 XX
 PS Claim 13; Page 28-30; 104pp; German.
 XX
 CC The invention relates to a method for inhibiting expression of a target
 CC gene (ABL91686-ABL91797) in a cell by introducing at least one
 CC oligoribonucleotide that has a double-stranded structure consisting of at
 CC most 49 sequential nucleotide pairs, with at least part of one strand
 CC complementary with the target gene and has at least one end a single-
 CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
 CC antisense inhibition of gene expression useful e.g. for treating tumours

CC but the oligoribonucleotides may also be directed against genes present
 CC in pathogens (e.g. plasmodium or viruses/viroids, pathogenic on humans,
 CC animals or plants) or against cytokine, id, developmental or prion genes.
 CC The method provides more effective inhibition of gene expression than use
 CC of known oligonucleotides, probably because the unpaired overhang
 CC increases stability and thus intracellular concentration
 XX
 SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 6; Length 3840;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GTGACATTTTCACGGCCATAGCGAA 25
 DB 1484 GTGACATTTTCACGGCCATAGCGAA 1460
 Search completed: February 9, 2005, 16:05:58
 Job time : 245.69 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds
(without alignments)
539.601 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 25

Sequence: 1 ggcagatttcacggcgcacgcgaa 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 287871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubna/US09_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubna/US10_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	25	100.0	219	16	US-10-029-386-15991
2	25	100.0	584	16	US-10-029-386-2291
3	25	100.0	2307	9	US-09-805-020-31
4	25	100.0	3840	18	US-10-384-339C-10
5	25	100.0	3860	9	US-09-866-866A-1
6	25	100.0	3860	9	US-09-866-866A-3
7	25	100.0	4533	9	US-09-805-020-30
8	25	100.0	4643	13	US-10-072-621-2
9	25	100.0	4643	14	US-10-097-340-1
10	25	100.0	4643	15	US-10-007-925A-258
11	25	100.0	4646	11	US-09-968-007A-459

c 12	25	100.0	4646	11	US-09-968-007A-747	Sequence 747, App
c 13	25	100.0	4646	17	US-10-641-653-1167	Sequence 1167, App
c 14	25	100.0	4646	17	US-10-343-657-1	Sequence 1, Appl1
c 15	25	100.0	4646	18	US-10-775-169-198	Sequence 198, App
c 16	25	100.0	4669	18	US-10-680-516-1	Sequence 1, Appl1
c 17	25	100.0	8630	9	US-09-306-417-1	Sequence 1, Appl1
c 18	25	100.0	8630	9	US-09-306-417-2	Sequence 2, Appl1
c 19	23.4	93.6	4317	13	US-10-044-671-1	Sequence 1, Appl1
c 20	23.4	93.6	4317	18	US-10-896-634-1	Sequence 1, Appl1
c 21	21.8	87.2	3852	17	US-10-101-433A-1	Sequence 1, Appl1
c 22	21.8	87.2	4186	15	US-10-619-359A-1	Sequence 1, Appl1
c 23	21.8	87.2	4189	9	US-09-866-866A-5	Sequence 5, Appl1
c 24	21.8	87.2	4195	17	US-10-619-359A-3	Sequence 3, Appl1
c 25	21.8	87.2	4254	17	US-10-388-934-265	Sequence 265, App
c 26	21.8	87.2	4254	17	US-10-352-319A-1464	Sequence 1464, App
c 27	21.8	87.2	4254	17	US-10-352-319A-1464	Sequence 32, Appl
c 28	21.8	87.2	4298	18	US-10-335-053-32	Sequence 1, Appl1
c 29	21.8	87.2	4369	9	US-09-769-097-1	Sequence 3, Appl1
c 30	21.8	87.2	4425	9	US-09-769-097-3	Sequence 7, Appl1
c 31	21.8	87.2	4788	9	US-09-866-866A-7	Sequence 11474, A
c 32	19	76.0	398	18	US-10-357-930-11474	Sequence 2305, App
c 33	19	76.0	416	18	US-10-357-930-2305	Sequence 430, App
c 34	19	76.0	490	15	US-10-102-524-430	Sequence 32646, A
c 35	19	76.0	539	18	US-10-357-930-32646	Sequence 41572, A
c 36	19	76.0	539	18	US-10-357-930-41572	Sequence 344, App
c 37	19	76.0	582	15	US-10-097-340-56	Sequence 56, Appl
c 38	19	76.0	2807	14	US-10-177-293-75	Sequence 75, Appl
c 39	19	76.0	2807	15	US-10-177-293-75	Sequence 175, App
c 40	19	76.0	3321	9	US-09-825-294-175	Sequence 2253, App
c 41	19	76.0	3321	9	US-09-880-107-2253	Sequence 175, App
c 42	19	76.0	3321	14	US-10-076-816-50	Sequence 50, Appl
c 43	19	76.0	3321	14	US-10-097-340-58	Sequence 58, Appl
c 44	19	76.0	3321	14	US-10-097-340-58	Sequence 77, Appl
c 45	19	76.0	3321	15	US-10-177-293-77	

ALIGNMENTS

RESULT 1
US-10-029-386-15991
Sequence 15991, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMITCA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15991
LENGTH: 219
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR7.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
OTHER INFORMATION: NT HIT: M29432.1, EVALUE 1.00e-120
OTHER INFORMATION: SWISSPROT HIT: P08183, EVALUE 8.00e-33
OTHER INFORMATION: EST_HUMAN HIT: BG567305.1, EVALUE 1.10e+00
US-10-029-386-15991
Query Match 100.0%; Score 25; DB 16; Length 219;
Best local similarity 100.0%; Pred. No. 0.016;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 77 GTGACATTTTCACGGCCATAGCGAA 101

RESULT 2
US-10-029-386-2291
; Sequence 2291, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMITC-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2291
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR7.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: NT HIT: M29432.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P08183, EVALUE 4.00e-32
US-10-029-386-2291

Query Match 100.0%; Score 25; DB 16; Length 584;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 320 GTGACATTTTCACGGCCATAGCGAA 344

RESULT 3
US-09-805-020-31/C
; Sequence 31, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Zurlic
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2307)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-31

Query Match 100.0%; Score 25; DB 9; Length 2307;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25

Db 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 4
US-10-384-339C-30/C
; Sequence 30, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Krentzler, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GEN
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 3840
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: mdr-1
; PATENT DOCUMENT NUMBER: AF016535
US-10-384-339C-30

Query Match 100.0%; Score 25; DB 18; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1484 GTGACATTTTCACGGCCATAGCGAA 1460

RESULT 5
US-09-866-866A-1/C
; Sequence 1, Application US/09866866A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-866A-1

Query Match 100.0%; Score 25; DB 9; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25

Db 1487 GTGACATTTTCACGGCCATAGCGAA 1463

RESULT 6
US-09-866-866A-3/C

Sequence 3, Application US/09866866A
Patent No. US2002010224A1
GENERAL INFORMATION:
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-022CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 3860
TYPE: DNA
ORGANISM: homo sapiens
US-09-866-866A-3

Query Match 100.0%; Score 25; DB 9; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1487 GTGACATTTTCACGGCCATAGCGAA 1463

RESULT 7

US-09-805-020-30/C
Sequence 30, Application US/09805020
Publication No. US20020086384A1
GENERAL INFORMATION:
APPLICANT: Levine, Zuzit
TITLE OF INVENTION: SPICE VARIANTS OF ONCOGENES
FILE REFERENCE: 2786-0168P
CURRENT APPLICATION NUMBER: US/09/805,020
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 4533
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(4533)
OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-30

Query Match 100.0%; Score 25; DB 9; Length 4533;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 8

US-10-072-621-2/C
Sequence 2, Application US/10072621
Publication No. US20020169137A1

GENERAL INFORMATION:
APPLICANT: Reiner, Peter B.
APPLICANT: Connop, Bruce P.
APPLICANT: Pollard, Michelle
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
FILE REFERENCE: 100103.402
CURRENT APPLICATION NUMBER: US/10/072,621
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
US-10-072-621-2

Query Match 100.0%; Score 25; DB 13; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATAGCGAA 25
Db 1908 GTGACATTTTCACGGCCATAGCGAA 1884

RESULT 9

US-10-097-340-1/C
Sequence 1, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAPARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVARTS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHWANDT
APPLICANT: Xumei ZHAO
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Title Of Invention: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
US-10-097-340-1

Query Match 100.0%; Score 25; DB 14; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1908 GTGACATTTTCACGGCCATAGCGAA 1884

RESULT 10
US-10-007-926A-258/c
Sequence 258, Application US/10007926A
Publication No. US20030143539A1
GENERAL INFORMATION:

APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOUIGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FEET, VINCENT

TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

FILE REFERENCE: 1546-R-00

CURRENT APPLICATION NUMBER: US/10/007,926A

PRIOR FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: 60/254,090

NUMBER OF SEQ ID NOS: 468

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 258

LENGTH: 4643

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: acp-binding cassette, sub-family b

OTHER INFORMATION: (mdr/cap, member 1 (ABCB1) gene.

US-10-007-926A-258

Query Match 100.0%; Score 25; DB 15; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1908 GTGACATTTTCACGGCCATAGCGAA 1884

RESULT 11
US-09-968-007A-459/c
Sequence 459, Application US/09968007A
Publication No. US20040115625A1
GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/09/968,007A
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,316
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: Patent In version 3.0

SEQ ID NO 459
LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
US-09-968-007A-459

Query Match 100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 12
US-09-968-007A-747/c
Sequence 747, Application US/09968007A
Publication No. US20040115625A1
GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat

TITLE OF INVENTION: Gene Sets

FILE REFERENCE: 689290-71

CURRENT APPLICATION NUMBER: US/09/968,007A

PRIOR FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US/60/237,172

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: US/60/237,173

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: US/60/237,278

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: US/60/237,294

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: US/60/237,295

PRIOR FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: US/60/237,316

NUMBER OF SEQ ID NOS: 1001

SOFTWARE: Patent In version 3.0

SEQ ID NO 747

LENGTH: 4646

TYPE: DNA

ORGANISM: Homo sapiens

US-09-968-007A-747

Query Match 100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGACATTTTCACGGCCATAGCGAA 25
DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 13
US-10-641-643-1167/c
Sequence 1167, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.
Jeffrey J. Seilhamer
Susan G. Stuart

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL

TITLE OF INVENTION: GENE EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/641,643
 FILING DATE: 14-Aug-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1167:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4646 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9187468
 SEQUENCE DESCRIPTION: SEQ ID NO: 1167 :
 US-10-641-643-1167

Query Match 100.0%; Score 25; DB 17; Length 4646;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
 DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 14
 US-10-343-657-1/c
 ; Sequence 1, Application US/10343657
 ; Publication No. US2004008682A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruth, Adam
 ; APPLICANT: Robinson, Igor B.
 ; TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that improve its
 ; TITLE OF INVENTION: Ability to Confer Resistance to Chemotherapeutic Drugs
 ; FILE REFERENCE: 00,616-A
 ; CURRENT APPLICATION NUMBER: US/10/343,657
 ; CURRENT FILING DATE: 2003-10-17
 ; PRIOR APPLICATION NUMBER: 60/222,313
 ; PRIOR FILING DATE: 2000-08-01
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 4646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (425)..(4264)
 ; US-10-343-657-1

Query Match 100.0%; Score 25; DB 17; Length 4646;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
 DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

RESULT 15

US-10-775-169-198/c
 ; Sequence 198, Application US/10775169
 ; Publication No. US20040175743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Burczynski, Michael
 ; APPLICANT: Twine, Natalie
 ; APPLICANT: Dornier, Andrew
 ; APPLICANT: Trepicchio, William
 ; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
 ; FILE REFERENCE: AM101080 (031896-013000)
 ; CURRENT APPLICATION NUMBER: US/10/775,169
 ; CURRENT FILING DATE: 2004-02-11
 ; NUMBER OF SEQ ID NOS: 5278
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 198
 ; LENGTH: 4646
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-775-169-198

Query Match 100.0%; Score 25; DB 18; Length 4646;
 Best Local Similarity 100.0%; Pred. No. 0.028;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACATTTTCACGGCCATAGCGAA 25
 DB 1911 GTGACATTTTCACGGCCATAGCGAA 1887

Search completed: February 9, 2005, 22:26:40
 Job time : 267.667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds
(without alignments)
388.593 Million cell updates/sec

Title: US-10-007-255-13

Perfect score: 25

Sequence: 1 gtgacatttcacggccatgacgaa 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsa1:*
- 9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	570	5	BP220580 BP220580
2	25	100.0	3843	9	AY408954 Homo sapi
3	25	100.0	3843	9	AY408955 Pan trogl
4	23.4	93.6	929	5	BO882401 AGENCOURT
5	21.8	87.2	485	6	CB727009 AMGNMUC:N
6	21.8	87.2	784	4	BI184814 UNL-P-FN-
7	21.8	87.2	894	2	BF584668 60208406
8	21.8	87.2	3182	3	AK030328 Mus muscu
9	21.8	87.2	3816	9	AY408956 Mus muscu
10	20.2	80.8	411	9	CL388323 RPI144 28
11	20.2	80.8	674	5	BU437349 60414518
12	20.2	80.8	716	5	BU239912 603322470
13	19.8	79.2	578	5	BP261688 BP261688
14	19.8	79.2	923	6	CD251708 AGENCOURT
15	19.8	79.2	1235	4	BM542792 AGENCOURT
16	19.2	76.8	432	1	AJ654223
17	19.2	76.8	448	6	CA780376 MP384 6
18	19.2	76.8	448	6	CA780376 MP384 6
19	19.2	76.8	535	5	BK678520 BX678520
20	19.2	76.8	582	5	BP193611 BP193611
21	19.2	76.8	588	7	CF359931 821214 MA
22	19.2	76.8	604	2	CK459590 929792 MA
23	19.2	76.8	608	2	BE291003 601084181
24	19.2	76.8	665	7	CN157996 946753 MA

C 25	19.2	76.8	665	7	CN159932	949057 MA
C 26	19.2	76.8	672	4	BI092416	BI092416 60285693
C 27	19.2	76.8	710	7	CK460832	CK460832 931149 MA
C 28	19.2	76.8	730	7	CK460130	CK460130 930381 MA
C 29	19.2	76.8	772	4	BG915267	BG915267 602814579
C 30	19.2	76.8	831	4	BI660209	BI660209 603302136
C 31	19.2	76.8	852	4	BI181199	BI181199 UNL-P-FN-
C 32	19.2	76.8	858	2	BE913573	BE913573 601667516
C 33	19.2	76.8	984	4	BI661427	BI661427 603304721
C 34	19.2	76.8	984	4	BI409869	BI409869 602962207
C 35	19.2	76.8	333	1	AJ524590	AJ524590 6043508.X
C 36	19.2	76.8	366	1	BM856196	BM856196 K-EST0139
C 37	19.2	76.8	371	1	AV695293	AV695293 AV695293
C 38	19.2	76.8	405	1	AJ921934	AJ921934 wmb6h05.X
C 39	19.2	76.8	411	8	AQ194986	AQ194986 RPI11-57
C 40	19.2	76.8	421	4	BM719759	BM719759 UI-E-EJ1-
C 41	19.2	76.8	426	4	BM684114	BM684114 UI-E-EJ1-
C 42	19.2	76.8	429	8	AQ194770	AQ194770 RPI11-57
C 43	19.2	76.8	434	1	AV648804	AV648804 AV648804
C 44	19.2	76.8	481	5	BO028054	BO028054 UI-H-CO-
C 45	19.2	76.8	501	1	AU149941	AU149941 AU149941

ALIGNMENTS

RESULT 1
BP220580/c
LOCUS
DEFINITION BP220580 Sugano cDNA library, colon Homo sapiens cDNA clone
COL03695, mRNA sequence.
ACCESSION BP220580
VERSION BP220580.1 GI:52093485
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL03695"
/tissue_type="colon"
/clone_lib="Sugano cDNA library, colon"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATGCGAA 25
|||||
Db 92 GTGACATTTTCACGGCCATGCGAA 68
|||||

RESULT 2
AY408954/c
LOCUS
DEFINITION AY408954 Homo sapiens ABCB1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY408954 GI:39764922
 VERSION AY408954.1
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 3843)
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 3843)
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES
 source
 1..3843
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>3843
 /gene="ABCB1"
 /locus_tag="HCM3396"
 ORIGIN
 Query Match 100.0%; Score 25; DB 9; Length 3843;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GTGACATTTTCACGGCCATAGCGAA 25
 Db 1487 GTGACATTTTCACGGCCATAGCGAA 1463
 RESULT 3
 AY408955/c
 LOCUS Pan troglodytes ABCB1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY408955
 VERSION AY408955.1 GI:39764923
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 REFERENCE 1 (bases 1 to 3843)
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 3843)
 AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES
 source
 1..3843
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
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 /gene="ABCB1"
 /locus_tag="HCM3396"
 ORIGIN
 Query Match 100.0%; Score 25; DB 9; Length 3843;
 Best Local Similarity 100.0%; Pred. No. 0.37;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GTGACATTTTCACGGCCATAGCGAA 25
 Db 1487 GTGACATTTTCACGGCCATAGCGAA 1463
 RESULT 4
 B0882401/c
 LOCUS AGENCOURT 8627902 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6291782 5', mRNA sequence.
 DEFINITION B0882401
 ACCESSION B0882401.1 GI:22274409
 VERSION B0882401.1
 KEYWORDS EST.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 929)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM2492 row: C column: 15
 High quality sequence stop: 677.
 FEATURES
 source
 1..929
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6291782"
 /issue_type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_43"
 /note="Organ: eye; Vector: pOTB7, Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"
 ORIGIN
 Query Match 93.6%; Score 23.4; DB 5; Length 929;
 Best Local Similarity 96.0%; Pred. No. 1.7;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GTGACATTTTCACGGCCATAGCGAA 25

Db 753 GTGACATTTTCAGCGCCATAGCGAA 729

RESULT 5 CB8727009/c 485 bp mRNA linear EST 11-APR-2003

LOCUS AMENNC:NRH5-00278-B7-A W Rat hypothalamus (10471) Rattus
DEFINITION norvegicus cDNA clone nrh5-00278-b7 5', mRNA sequence.

ACCESSION CB8727009
VERSION CB8727009.1 GI:29793993

KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus

REFERENCE 1 (bases 1 to 485)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00278 row: b column: 7.
Location/Qualifiers

FEATURES
source 1..485
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrh5-00278-b7"
/clone_lib="W Rat hypothalamus (10471)"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat
hypothalamus adult female Wistar rat avg. insert size 2.3
kb fraction 6 and 7"

ORIGIN

Query Match 87.2%; Score 21.8; DB 6; Length 485;
Best Local Similarity 92.0%; Pred. No. 9.5;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCAGCGCCATAGCGAA 25
Db 239 GTGACGTTTTCGCGCCATAGCGAA 215

RESULT 6 B1184814 784 bp mRNA linear EST 10-JUL-2001
LOCUS B1184814
DEFINITION UNL-P-FN-cr-g-09-0-UNL.61 UNL-P-FN Sus scrofa cDNA clone
UNL-P-FN-cr-g-09-0-UNL 3', mRNA sequence.
ACCESSION B1184814
VERSION B1184814.1 GI:14659223
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
1 (bases 1 to 784)
Caetano, A.R., Johnson, R.K. and Pomp, D.
Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
Mamm. Genome 14 (1), 65-70 (2003)

REFERENCE 1 (bases 1 to 784)
AUTHORS Caetano, A.R., Johnson, R.K. and Pomp, D.
TITLE Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles
JOURNAL Mamm. Genome 14 (1), 65-70 (2003)

JOURNAL MEDLINE
PUBMED
COMMENT Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu

Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
POLYA=No.

FEATURES
source Location/Qualifiers

1..784
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="University of Nebraska, Lincoln Swine Selection
Lines"

/db_xref="taxon:9823"
/clone="UNL-P-FN-cr-g-09-0-UNL"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"

/clone_lib="UNL-P-FN"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
library is a normalized library representing porcine
ovarian follicles, ranging between 2.0 to 10.0 mm in
diameter, collected during 7 days of the follicular phase
of the pig estrous cycle. This library was derived from
the library UNL-P-F2. The tag is a string of 5-6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996.
TAG_SEQ=None found"

ORIGIN

Query Match 87.2%; Score 21.8; DB 4; Length 784;
Best Local Similarity 92.0%; Pred. No. 10;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCAGCGCCATAGCGAA 25
Db 201 GTGACATTTTCGCGCCATAGCGAA 225

RESULT 7 BF584668 894 bp mRNA linear EST 12-DEC-2000
LOCUS BF584668
DEFINITION 602098406F1 NCI CGAP_C024 Mus musculus cDNA clone IMAGE:421855 5',
mRNA sequence.
ACCESSION BF584668
VERSION BF584668.1 GI:11658386
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 894)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contract: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LHAM9798 row: 1 column: 02
High quality sequence stop: 651.
Location/Qualifiers

FEATURES
source

1..894
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4218385"
/lab_host="DH10B (T1 phage-resistant)"

ORIGIN

/clone_lib="NCI CGAP Co24"
 /note="Organ: Cloned; Vector: pCMV-SPORT6; Site: 1; Not1;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP Library."

Query Match

Best Local Similarity 92.0%; Pred. No. 11;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1 GTGACATTTTCAGCGCCATAGCGAA 25
 491 GTGACATCTTCTCGGCATAGCGAA 467

Db

RESULT 8
 AK030328/c 3182 bp mRNA linear HTC 03-APR-2004
 LOCUS
 DEFINITION Mus musculus 11 days pregnant adult female ovary and uterus cDNA,
 RIKEN full-length enriched library, clone:5031438E12
 product:ARP-binding cassette, sub-family B (MDR/TAP), member 1B,
 full insert sequence.

ACCESSION

AK030328
 AK030328.1 GI:26081769

VERSION

HTC; CAP trapper.

KEYWORDS

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1

AUTHORS

Carninci, P. and Hayashizaki, Y.

TITLE

High-efficiency full-length cDNA cloning

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

MEDLINE

99279253

PUBMED

10349636

REFERENCE

2

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE

Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL

Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE

2049374

PUBMED

11042159

REFERENCE

3

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kikunaka, T., Tashiro, H., Itoh, M.,
 Sun, N., Ishii, Y., Nakamura, S., Hazama, S., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE

RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer

JOURNAL

Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE

20530913

PUBMED

11076861

REFERENCE

4

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.

TITLE

Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

JOURNAL

5

AUTHORS

The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.

TITLE

Analyses of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL

6 (bases 1 to 3182)

AUTHORS

Adachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
 Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishih, K., Nomura, K., Numazaki, R., Ono, M., Ohata, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogawa, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Kahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.

TITLE

Direct Submission
 Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
 Location/Qualifiers

FEATURES

source
 1..3182
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="PANTOM:DB:5031438E12"
 /db_xref="taxon:10090"
 /clone="5031438E12"
 /sex="female"
 /tissue_type="ovary and uterus"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="11 days pregnant adult"
 1..3182
 /note="ARP-binding cassette, sub-family B (MDR/TAP),
 member 1B (MGD|MG1:97568, GBI|NM_011075, evidence: BLASTN,
 99%, match=2587)"

misc_feature

1..3182

ORIGIN

Query Match 87.2%; Score 21.8; DB 3; Length 3182;
 Best Local Similarity 92.0%; Pred. No. 14;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

1 GTGACATTTTCAGCGCCATAGCGAA 25
 1576 GTGACATCTTCTCGGCATAGCGAA 1552

Db

RESULT 9
 AY408956/c 3816 bp DNA linear GSS 15-DEC-2003
 LOCUS
 DEFINITION Mus musculus ABCB1 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION
 AY408956
 VERSION
 AY408956.1 GI:39764924
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 3816)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Perletera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 3816)

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL

Science 302 (5652), 1960-1963 (2003)

AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
 Perletera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
 Adams, M.D. and Cargill, M.

PUBMED

14671302

REFERENCE

2 (bases 1 to 3816)

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/db_xref="caxon:98231"
/clone="RPCI44_284D11"
/sex="male"
/cell_type="blood"
/clone_1ib="RPCI-44"
/notes="Vector: pTRABAC2; Site_1: EcoRI; Site_2: EcoRI; porcine male BAC library produced by Pieter de Jong"

ORIGIN

Query Match      80.8%; Score 20.2; DB 9; Length 411;
Best Local Similarity 88.0%; Pred. No. 57;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY
Db      271 GTGACATTTCCACGGCCGTACGAA 295
      |||||||
1 GTGACATTTTCACGCCATATCGAA 25
      |||||||

RESULT 11
LOCUS       BU437349/c      674 bp      mRNA      linear      EST 29-NOV-2002
DEFINITION  604145918F1 CSEQRBN11 Gallus gallus cDNA clone CHEST986c5 5', mRNA
LOCUS      BU437349
ACCESSION  BU437349
VERSION    BU437349.1 GI:25926660
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
            1 (bases 1 to 674)
REFERENCE   Boardman,P.B., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
AUTHORS    Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE       A Comprehensive Collection of Chicken CDNAs
JOURNAL     Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE    22335534
PUBMED     12443392
COMMENT    Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
            Location/Qualifiers
                1..674
                /organism="Gallus gallus"
                /mol_type="mRNA"
                /strain="layer and broiler"
                /db_xref="taxon:9031"
                /clone="CHEST986c5"
                /sex="Male and female"
                /tissue_type="muscle"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_1ib="CSEQRBN11"
                /notes="Vector: pBluescript II KS(+); Site_1: EcoRI;
                Site_2: NotI; This normalized library was constructed from
                1 million independent clones. cDNA synthesis was initiated
                using an oligo(dT) primer, using methylated C in the first
                strand synthesis reaction. Following this first strand
                reaction, double-stranded cDNA was blunt-ended, ligated to
                NotI adapters, digested with EcoRI, size-selected, and
                cloned into the NotI and EcoRI compatible sites of a
                custom modified MCS of the pBluescript (KS+) vector. The
                library was normalized in 2 rounds using conditions
                adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
                Bonaldo et al., Genome Research 6 (1996): 791, except that
                a significantly longer reannealing hybridization was
                used."

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Query Match 80.8%; Score 20.2; DB 5; Length 674;
 Best Local Similarity 88.0%; Pred. No. 63;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATACGGA 25
 |||||
 Db 237 GTGACATCTCTACGGCCATACGGA 213

RESULT 12
 BU239912/c 716 bp mRNA linear EST 26-NOV-2002
 LOCUS 603322470F1 CSEQCHN33 Gallus gallus cDNA clone CHEST250K17 5', mRNA
 DEFINITION

ACCESSION BU239912
 VERSION BU239912.1 GI:25485977
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 1 (bases 1 to 716)
 E-mail: Simon.Hubbard@umist.ac.uk.

REFERENCE Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.,
 A Comprehensive Collection of Chicken cDNAs
 CURT. BIOL. 12 (22), 1965-1969 (2002)
 22335534
 12445392
 MEDLINE
 PUBMED

COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source location/Qualifiers
 1..716

/organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton line 151"
 /db_xref="taxon:9031"
 /clone="CHEST250K17"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN33"
 /note="Organ: liver; Vector: pluescript II KS(+); Site_1:
 EcorI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dt) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with
 EcorI, size-selected, and cloned into the NotI and EcorI
 compatible sites of a custom modified MCS of the
 pluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldi et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 80.8%; Score 20.2; DB 5; Length 716;
 Best Local Similarity 88.0%; Pred. No. 64;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGACATTTTCACGGCCATACGGA 25
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 Db 506 GTGACATCTCTACGGCCATACGGA 482

RESULT 13
 BP261688/c 578 bp mRNA linear EST 16-SEP-2004
 LOCUS BP261688 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION

ACCESSION BP261688
 VERSION BP261688.1 GI:52176919
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 578)
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source location/Qualifiers
 1..578

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HS104571"
 /tissue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Query Match 79.2%; Score 19.8; DB 5; Length 578;
 Best Local Similarity 91.3%; Pred. No. 97;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGACATTTTCACGGCCATACGGA 24
 |||||
 Db 545 TGACATTTTCACGGCCATACGGA 523

RESULT 14
 CD251708/c 923 bp mRNA linear EST 22-MAY-2003
 LOCUS CD251708
 DEFINITION

ACCESSION AGENCOURT_14205957 NIH_MGC_179 Homo sapiens cDNA clone
 IMAGE:30384175 5', mRNA sequence.
 CD251708
 CD251708.1 GI:31012174
 EST.

ORGANISM Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 923)
 NIH-MGC http://imgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: g9apbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein
 cDNA Library Preparation: Invitrogen Corp
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: NDAM49 row: d column: 08
 High quality sequence start: 2

FEATURES High quality sequence stop: 463.
Location/Qualifiers
1. .923

/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="IMAGE:30384175"
/issue_type="Pituitary"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_1ib="NIH_MGC_179"
/note="Organ: brain; Vector: PCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC library."

ORIGIN

Query Match 79.2%; Score 19.8; DB 6; Length 923;
Best Local Similarity 91.3%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACATTTTCACGGCCATAGCGA 24
|||||
DB 580 TGACATTTTCACGGCCATAGCGA 558

RESULT 15
BM542792 1235 bp mRNA linear EST 20-FEB-2002
LOCUS BM542792.1
DEFINITION AGENCOURT_6426041 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5520790

ACCESSION BM542792
VERSION BM542792.1 GI:18772622
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 1235)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLAM12185 row: f column: 23
High quality sequence stop: 495.
Location/Qualifiers

FEATURES
source 1. .1235

/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="IMAGE:5520790"
/issue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_71"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

ORIGIN

Query Match 79.2%; Score 19.8; DB 4; Length 1235;
Best Local Similarity 91.3%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACATTTTCACGGCCATAGCGA 24

DB 529 TGACATTTTCACGGCCATAGCGA 507
|||||

Search completed: February 9, 2005, 21:55:42
Job time : 2450.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW nucleic - nucleic search, using SW model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds
(without alignments)
2517.530 Million cell updates/sec

Title: US-10-007-255-14

Perfect score: 25
Sequence: 1 cgaaccaggcagcgtcgaatgcga 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

GenBank:
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_seg:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX504311 Sequence
2	25	100.0	25	6	AX504328 Sequence
3	25	100.0	215	9	HUMMDR1A12
4	25	100.0	2726	6	I33621
5	25	100.0	3840	6	AX481416
6	25	100.0	3843	6	BD171402
7	25	100.0	3852	9	AF537133
8	25	100.0	3852	9	AF537134
9	25	100.0	3852	9	AF582534
10	25	100.0	3860	6	AX322787
11	25	100.0	3860	6	AX322789
12	25	100.0	3924	6	BD190395
13	25	100.0	3924	6	BD234199
14	25	100.0	3924	6	AR380623
15	25	100.0	3924	6	AR452557
16	25	100.0	3924	6	AX024455
17	25	100.0	3924	6	AX409652
18	25	100.0	3924	9	HUMMDR3
19	25	100.0	3988	6	BD190394

c	20	25	100.0	3988	6	AR452556	AR452556 Sequence
c	21	25	100.0	3988	6	AX024454	AX024454 Sequence
c	22	25	100.0	4186	6	AR399194	AR399194 Sequence
c	23	25	100.0	4186	6	AX108654	AX108654 Sequence
c	24	25	100.0	4192	9	AF016535	AF016535 Homo sapi
c	25	25	100.0	4195	6	AR399195	AR399195 Sequence
c	26	25	100.0	4195	6	AX108656	AX108656 Sequence
c	27	25	100.0	4264	6	AR051647	AR051647 Sequence
c	28	25	100.0	4264	6	AR051650	AR051650 Sequence
c	29	25	100.0	4378	6	BD2326	BD2326 Multidrug r
c	30	25	100.0	4553	6	CO716151	CO716151 Sequence
c	31	25	100.0	4643	6	CQ815440	CQ815440 Sequence
c	32	25	100.0	4643	6	AX522070	AX522070 Sequence
c	33	25	100.0	4643	6	AX587788	AX587788 Sequence
c	34	25	100.0	4646	6	BD234195	BD234195 ATP-Bind
c	35	25	100.0	4646	6	CO861565	CO861565 Sequence
c	36	25	100.0	4646	6	I49610	I49610 Sequence 2
c	37	25	100.0	4646	6	AR380622	AR380622 Sequence
c	38	25	100.0	4646	6	AX336420	AX336420 Sequence
c	39	25	100.0	4646	6	AX336708	AX336708 Sequence
c	40	25	100.0	4646	6	AX391099	AX391099 Sequence
c	41	25	100.0	4646	6	AX504298	AX504298 Sequence
c	42	25	100.0	4646	9	HUMMDR1	M14758 Homo sapien
c	43	25	100.0	4669	6	AR055785	AR055785 Sequence
c	44	25	100.0	4669	6	AR091275	AR091275 Sequence
c	45	25	100.0	4669	6	I08557	I08557 Sequence 3

ALIGNMENTS

RESULT 1	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
LOCUS	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
DEFINITION	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
ACCESSION	AX504311	Sequence 14 from Patent WO0234291.	25 bp	DNA	linear	PAT 27-SEP-2002
VERSION	AX504311.1	GI:23386129	25 bp	DNA	linear	PAT 27-SEP-2002
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
Q						
Y						
Db						
RESULT 2						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						

REFERENCE 1
AUTHORS Colgan, S.P.
TITLE Compositions and methods for treating hematologic malignancies and multiple drug resistance
JOURNAL Patent: WO 0234291-A 31 02-MAY-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
FEATURES Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGCGCA 25
Db 25 CGAACGAGGCGACGTGCATGCGCA 1

RESULT 3
LOCUS HUMMDR1A12 215 bp DNA linear PRI 08-JAN-1995
DEFINITION Human P-glycoprotein (MDR1) gene, exon 14.
ACCESSION M29433.1 J05168
VERSION M29433.1 GI:187482
KEYWORDS P-glycoprotein; multidrug resistance.
SEGMENT 12 of 26
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 215)
AUTHORS Chen, C.J., Clark, D., Ueda, K., Pastan, I., Gottesman, M.M. and Roninson, I.B.
TITLE Genomic organization of the human multidrug resistance (MDR1) gene and origin of P-glycoproteins
JOURNAL J. Biol. Chem. 265 (1), 506-514 (1990)
MEDLINE 9009448
PubMed 1967175
COMMENT Original source text: Human multidrug resistant cell line KB-VL DNA.
Draft entry and computer-readable sequence for [1] kindly submitted by I.B. Roninson, 27-OCT-1989.
FEATURES Location/Qualifiers
source 1..215
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="7q21"
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/gene="PGY1"
/note="PGY1 mRNA and introns"
intron <1..17
/gene="PGY1"
/note="PGY1, intron M"
exon 18..188
/gene="PGY1"
/note="P-glycoprotein; G00-120-712"
/number=14
189..>215
/gene="PGY1"
/note="PGY1, intron N"

ORIGIN
Query Match 100.0%; Score 25; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGCGCA 25
Db 103 CGAACGAGGCGACGTGCATGCGCA 79

RESULT 4
LOCUS I33621 2726 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5593840.
ACCESSION I33621
VERSION I33621.1 GI:1824412
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2726)
AUTHORS Bhattachar, S.K., George, A.L. Jr. and Nazarenko, I.
TITLE Amplification of nucleic acid sequences
JOURNAL Patent: US 5593840-A 1 14-JAN-1997;
FEATURES Location/Qualifiers
source 1..2726
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 2726;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGCGCA 25
Db 144 CGAACGAGGCGACGTGCATGCGCA 120

RESULT 5
LOCUS AX481416 3840 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 30 from Patent WO02055693.
ACCESSION AX481416
VERSION AX481416.1 GI:22316330
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P.
TITLE Method for inhibiting the expression of a target gene
JOURNAL Patent: WO 02055693-A 30 18-JUL-2002;
Ribopharma AG (DE)
FEATURES Location/Qualifiers
source 1..3840
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGCGCA 25
Db 1637 CGAACGAGGCGACGTGCATGCGCA 1613

RESULT 6
LOCUS BD171402 3843 bp DNA linear PAT 18-FEB-2003
DEFINITION Method for predicting side effects of immunosuppressant and primer used therefor.
ACCESSION BD171402
VERSION BD171402.1 GI:28412692

KEYWORDS JP 2002223769-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3843)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2002223769-A/1
PD 13-AUG-2002
PF 31-JAN-2001 JP 2001024723
PI ICHIRO IEIRI
PC C12N15/09, C12N15/68, C12N15/00
CC Method for predicting side effects of immunosuppressant and
CC primer used
CC therefor
CH Key
FT source
FEATURES
source Location/Qualifiers
1..3843
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 3843;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAACCGGCGACGTCATGGCGA 25
DB 1640 CGAACCGGCGACGTCATGGCGA 1616
RESULT 7
AF537133/c 3852 bp mRNA linear PRI 11-SRP-2002
LOCUS Macaca mulatta multidrug resistance p-glycoprotein mRNA, complete
DEFINITION cds.
ACCESSION AF537133
VERSION AF537133.1 GI:22775295
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 3852)
AUTHORS Hanekom, S.R., Xiao, G. and Crespi, C.L.
JOURNAL Rhesus monkey P-glycoprotein mRNA
TITLE Unpublished
AUTHORS 2 (bases 1 to 3852)
JOURNAL Hanekom, S.R., Xiao, G. and Crespi, C.L.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2002) BD Biosciences, 6 Henshaw Street, Woburn,
MA 01801, USA
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAACCGGCGACGTCATGGCGA 25
DB 1649 CGAACCGGCGACGTCATGGCGA 1625
RESULT 8
AF537134 3852 bp mRNA linear PRI 06-JUN-2003
LOCUS Macaca fascicularis multidrug resistance p-glycoprotein mRNA,
DEFINITION complete cds.
ACCESSION AF537134
VERSION AF537134.2 GI:31442762
KEYWORDS
SOURCE
ORGANISM
Macaca fascicularis (crah-eating macaque)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 3852)
AUTHORS Stocker, P.J., Steimel-Crespi, D.T., Xiao, G. and Crespi, C.L.
JOURNAL Cynomolgous monkey P-glycoprotein mRNA
TITLE Unpublished
AUTHORS 2 (bases 1 to 3852)
JOURNAL Stocker, P.J., Steimel-Crespi, D.T., Xiao, G. and Crespi, C.L.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2002) BD Biosciences, 6 Henshaw Street, Woburn,
MA 01801, USA
REFERENCE 3 (bases 1 to 3852)
AUTHORS Stocker, P.J., Steimel-Crespi, D.T., Xiao, G. and Crespi, C.L.
JOURNAL Direct Submission
JOURNAL Submitted (06-JUN-2003) BD Biosciences, 6 Henshaw Street, Woburn,
MA 01801, USA
REMARK
COMMENT Sequence update by submitter
ON JUN 6, 2003 this sequence version replaced gi:22775297.
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Db 1649 CGAACGAGGCGACGTGCATGGCGA 1625

RESULT 9 3852 bp mRNA linear PRI 20-APR-2004
LOCUS AY582534/c
DEFINITION Macaca mulatta multidrug resistance protein (MDR1) mRNA, complete cds.

ACCESSION AY582534
KEYWORDS
SOURCE
ORGANISM Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.

REFERENCE
AUTHORS 1 (bases 1 to 3852)
TITLE Booth-Genthe, C.L., Roller, C.R. and Rushmore, T.H.
JOURNAL Cloning of Macaca mulatta MDR1
AUTHORS Unpublished
REFERENCE 2 (bases 1 to 3852)
TITLE Booth-Genthe, C.L., Roller, C.R. and Rushmore, T.H.
JOURNAL Direct Submission
TITLE Submitted (25-MAR-2004) Drug Metabolism, Merck Research
LABORATORIES, WP75A-203, West Point, PA 19486, USA

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Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
Db 1649 CGAACGAGGCGACGTGCATGGCGA 1625

RESULT 10 3860 bp DNA linear PAT 07-JAN-2002
LOCUS AX322787/c
DEFINITION Sequence 1 from Patent WO0192877.
ACCESSION AX322787
VERSION AX322787.1 GI:18093766
KEYWORDS

SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Sorrentino, B. and Schuetz, J.
JOURNAL Method of identifying and/or isolating stem cells
PATENT: WO 0192877/A1 06-DEC-2001;
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
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LOCUS AX322789/c
DEFINITION Sequence 3 from Patent WO0192877.
ACCESSION AX322789
VERSION AX322789.1 GI:18093767
KEYWORDS

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ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Sorrentino, B. and Schuetz, J.
TITLE Method of identifying and/or isolating stem cells
JOURNAL Patent: WO 0192877-A 3 06-DEC-2001;
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
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DB 1640 CGAACGAGGCGACGTGCATGGCGA 1616
RESULT 12
BD190395/c 3924 bp DNA linear PAT 17-JUL-2003
LOCUS Phosphatidylcholine as a medicament for the protection of mucosa.
DEFINITION BD190395
ACCESSION BD190395.1 GI:33000134
VERSION JP 2002522381-A/2.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 3924)
AUTHORS Strommel, W.
TITLE Phosphatidylcholine as a medicament for the protection of mucosa
JOURNAL Patent: JP 2002522381-A 2 23-JUL-2002;
Wolfgang Strommel
COMMENT OS Homo sapiens
PN JP 2002522381-A/2
PD 23-JUL-2002
PF 06-AUG-1999 JP 2000563262
PR 06-AUG-1998 DE 198 35 526.2,15-DEC-1998 DE 198 57 750.8 PI
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BD234199/c 3924 bp DNA linear PAT 17-JUL-2003
LOCUS ATP-binding cassette genes and proteins for diagnosis and remedy of
DEFINITION lipid disorders and inflammatory diseases.
ACCESSION BD234199
VERSION BD234199.1 GI:33043969
KEYWORDS JP 2002525111-A/9.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 3924)
TITLE Schmitz, G. and Klucken, J.
JOURNAL ATP-binding cassette genes and proteins for diagnosis and remedy of
lipid disorders and inflammatory diseases
Patent: JP 2002525111-A 9 13-AUG-2002;
BAYER AKTIENGESELLSCHAFT
FEATURES OS Homo sapiens (human)
SOURCE OS Homo sapiens (human)
PN JP 2002525111-A/9
PD 13-AUG-2002
PF 21-SEP-1999 JP 2000572359
PR 25-SEP-1998 US 60/101706
PI GERD SCHMITZ, JOCHEN KLUCKEN
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P3/06,A61P9/10, PC
A61P29/00,
PC C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
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PC G01N33/53,C12N15/00,C12N5/00,A61K37/02
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AR380623/c 3924 bp DNA linear PAT 18-DEC-2003
LOCUS AR380623
DEFINITION Sequence 1168 from patent US 6607879.
ACCESSION AR380623
VERSION AR380623.1 GI:40088257
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 Unclassified.
AUTHORS 1 (bases 1 to 3924)
TITLE Cocks, R.G., Stuart, S.G. and Seilhammer, J.J.
JOURNAL Compositions for the detection of blood cell and immunological
response gene expression
Patent: US 6607879-A 1168 19-AUG-2003;
FEATURES Location/Qualifiers
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RESULT 15
AR452557/c 3924 bp DNA linear PAT 20-FEB-2004
LOCUS AR452557
DEFINITION Sequence 2 from patent US 6677319.
ACCESSION AR452557

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VERSION      AR452557.1  GI:42684345
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 3924)
AUTHORS      Stremmel, W.
TITLE        Phosphatidylcholine as medication with protective effect large
JOURNAL      intestinal mucosa
FEATURES     Patent: US 6677319-A 2.13-JAN-2004;
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SUMMARIES

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C 1	25	100.0	2726	1 US-08-461-823-1	Sequence 1, Appl1
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C 3	25	100.0	3924	4 US-09-762-195-2	Sequence 2, Appl1
C 4	25	100.0	3988	4 US-09-762-195-1	Sequence 1, Appl1
C 5	25	100.0	4186	4 US-09-672-810-1	Sequence 1, Appl1
C 6	25	100.0	4195	4 US-09-672-810-3	Sequence 3, Appl1
C 7	25	100.0	4264	2 US-08-784-649A-1	Sequence 1, Appl1
C 8	25	100.0	4264	2 US-08-784-649A-5	Sequence 5, Appl1
C 9	25	100.0	4646	1 US-08-181-471-2	Sequence 2, Appl1
C 10	25	100.0	4646	4 US-09-023-655-1167	Sequence 1167, Ap
C 11	25	100.0	4669	2 US-08-583-276-18	Sequence 18, Appl
C 12	25	100.0	4669	2 US-08-752-447-1	Sequence 1, Appl1
C 13	25	100.0	4669	4 US-09-316-167-1	Sequence 1, Appl1
C 14	25	100.0	4669	4 US-09-397-233-1	Sequence 1, Appl1
C 15	25	100.0	4669	6 5206352-3	Sequence 1, Appl1
C 16	25	100.0	4669	6 5206352-3	Patent No. 5206352
C 17	25	100.0	6505	2 US-08-793-610-5	Sequence 5, Appl1
C 18	25	100.0	8630	4 US-09-306-417-1	Sequence 1, Appl1
C 19	25	100.0	8630	4 US-09-306-417-2	Sequence 2, Appl1
C 20	25	100.0	9318	2 US-08-793-610-6	Sequence 6, Appl1
C 21	21.8	87.2	4279	4 US-09-672-725C-1	Sequence 1, Appl1
C 22	21.8	87.2	4279	4 US-09-672-725C-2	Sequence 22, Appl
C 23	21.8	87.2	4279	4 US-09-672-725C-24	Sequence 24, Appl
C 24	21.8	87.2	4279	4 US-09-672-725C-26	Sequence 26, Appl
C 25	21.8	87.2	4317	4 US-09-672-725C-3	Sequence 3, Appl1
C 26	21.8	87.2	4317	4 US-10-044-671-1	Sequence 1, Appl1
C 27	20.2	80.8	4233	3 US-09-120-513-1	Sequence 1, Appl1

C 28	20.2	80.8	4233	3 US-09-450-105-1	Sequence 1, Appl1
C 29	18.6	74.4	4047	2 US-08-612-734B-1	Sequence 1, Appl1
C 30	18.6	74.4	4800	2 US-08-612-734B-3	Sequence 3, Appl1
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C 32	17.8	71.2	601	4 US-09-949-016-191243	Sequence 191243,
C 33	17.8	71.2	601	4 US-09-949-016-191244	Sequence 191244,
C 34	17.8	71.2	30847	4 US-09-949-016-16657	Sequence 16657, A
C 35	17.8	71.2	121970	4 US-09-949-016-17216	Sequence 17216, A
C 36	17.6	70.4	654	4 US-09-252-991A-9404	Sequence 9404, Ap
C 37	17.6	70.4	771	4 US-09-252-991A-9372	Sequence 9372, Ap
C 38	17.6	70.4	813	4 US-09-252-991A-9462	Sequence 9462, Ap
C 39	17.6	70.4	1110	4 US-09-328-352-7779	Sequence 2779, Ap
C 40	17.6	70.4	1341	4 US-09-902-540-7697	Sequence 7697, Ap
C 41	17.6	70.4	6404	4 US-09-902-540-760	Sequence 760, App
C 42	17.2	68.8	702	4 US-09-583-110-92	Sequence 92, Appl
C 43	17.2	68.8	708	4 US-09-107-433-1098	Sequence 1098, Ap
C 44	17.2	68.8	10690	3 US-08-961-527-93	Sequence 93, Appl
C 45	17.2	68.8	17907	4 US-09-949-016-13189	Sequence 13189, A

ALIGNMENTS

RESULT 1
US-08-461-823-1/c
Sequence 1, Application US/08461823
Patent No. 5593840
GENERAL INFORMATION:
APPLICANT: Bhatnagar, Satish K.
APPLICANT: George Jr., Albert L.
APPLICANT: Nazarenko, Irina
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: OncorPharm, Inc.
STREET: 200 Perry Parkway
CITY: Gaithersburg
STATE: Maryland
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08461,823
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/168,621
FILING DATE: 16-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,433
FILING DATE: 27-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Karta, Glenn E.
REGISTRATION NUMBER: 30,649
REFERENCE/DOCKET NUMBER: PA-0012 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301 527-2058
TELEFAX: 301 208-6997
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-461-823-1

Query Match 100.0%; Score 25; DB 1; Length 2726;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 144 CGAACGAGGCGACGTGCATGGCGA 120

RESULT 2

US-09-023-655-1168/c
Sequence 1168, Application US/09023655
Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: HEREWITH
APPLICATION NUMBER: US/09/023,655

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1168:

SEQUENCE CHARACTERISTICS:
LENGTH: 3924 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK
CLONE: g187501

US-09-023-655-1168

Query Match 100.0%; Score 25; DB 4; Length 3924;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 1678 CGAACGAGGCGACGTGCATGGCGA 1654

RESULT 3

US-09-762-195-2/c
Sequence 2, Application US/09762195
Patent No. 6677319
GENERAL INFORMATION:
APPLICANT: Stremmel, Wolfgang

TITLE OF INVENTION: Phosphatidylcholine as Medication with
TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
FILE REFERENCE: 34691/208520
CURRENT APPLICATION NUMBER: US/09/762,195
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/EP99702426
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 198 57 570.8 DE
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3924
TYPE: DNA
ORGANISM: Homo sapiens
US-09-762-195-2

OY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 1678 CGAACGAGGCGACGTGCATGGCGA 1654

RESULT 4

US-09-762-195-1/c
Sequence 1, Application US/09762195
Patent No. 6677319

GENERAL INFORMATION:
APPLICANT: Stremmel, Wolfgang
TITLE OF INVENTION: Phosphatidylcholine as Medication with
TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
FILE REFERENCE: 34691/208520
CURRENT APPLICATION NUMBER: US/09/762,195
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/EP99702426
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 198 57 570.8 DE
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3988
TYPE: DNA
ORGANISM: Homo sapiens
US-09-762-195-1

Query Match 100.0%; Score 25; DB 4; Length 3988;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 1706 CGAACGAGGCGACGTGCATGGCGA 1682

RESULT 5

US-09-672-810-1/c
Sequence 1, Application US/09672810
Patent No. 6617450

GENERAL INFORMATION:
APPLICANT: STOCKER, PENNY J.
APPLICANT: STEIMEL-CRESPI, DOROTHY T.
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810


```

CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 4186
TYPE: DNA
ORGANISM: Macaca fascicularis
FEATURE:
NAME/KEY: CDS
LOCATION: (100)...(3940)
US-09-672-810-1

Query Match          100.0%; Score 25; DB 4; Length 4186;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGCATGCAATGGCGA 25
Db 1739 CGAACGAGGCGCATGCAATGGCGA 1715

RESULT 6
US-09-672-810-3/c
Sequence 3, Application US/09672810
Patent No. 6617450
GENERAL INFORMATION:
APPLICANT: STOCKER, PENNY J.
APPLICANT: STEIMEL-CRESPI, DOROTHY T.
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 4195
TYPE: DNA
ORGANISM: Macaca fascicularis
FEATURE:
NAME/KEY: CDS
LOCATION: (100)...(3949)
US-09-672-810-3

Query Match          100.0%; Score 25; DB 4; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGCATGCAATGGCGA 25
Db 1748 CGAACGAGGCGCATGCAATGGCGA 1724

RESULT 7
US-08-784-649A-1/c
Sequence 1, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: SIKIC, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
```

```

STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-784-649A-1

Query Match          100.0%; Score 25; DB 2; Length 4264;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGCATGCAATGGCGA 25
Db 1778 CGAACGAGGCGCATGCAATGGCGA 1754

RESULT 8
US-08-784-649A-5/c
Sequence 5, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: SIKIC, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 5:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-784-649A-5

Query Match 100.0%; Score 25; DB 2; Length 4264;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 1778 CGAACGAGGCGACGTGCATGGCGA 1754

RESULT 9
US-08-181-471-2/c
Sequence 2, Application US/08181471
Patent No. 5641508
GENERAL INFORMATION:
APPLICANT: Li, Lingna
APPLICANT: Lishko, Valeryi K.
TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas Fitting
STREET: 12526 High Bluff Drive, Suite 300
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92130
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,471
FILING DATE: 13-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,553
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: ANT0029P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-792-3680
TELEFAX: 619-792-8477
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4267
US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAACGAGGCGACGTGCATGGCGA 25
|||||

DB 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 10
US-09-023-655-1167/c
Sequence 1167, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1167:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187468
US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 11
US-08-583-276-18/c
Sequence 18, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
APPLICANT: McDonagh, Kevin T.
APPLICANT: Nienhuis, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES
NUMBER OF SEQUENCES: 19

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Carella, Byrne, Bain, Gillilan,
;; ADDRESSEE: Cecchi & Stewart
;; STREET: 6 Becker Farm Road
;; CITY: Roseland
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07068
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch diskette
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: DM4 V2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/583,276
;; FILING DATE: 05-JAN-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/332,444
;; FILING DATE: 31-OCT-1994
;; APPLICATION NUMBER: 07/887,712
;; FILING DATE: 22-MAY-1992
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4669 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: singular
;; TOPOLOGY: linear
;; MOLECULE TYPE:
;; DESCRIPTION: Genomic DNA
;; US-08-583-276-18

Query Match 100.0%; Score 25; DB 2; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGAACGAGGCGACGTGCATGGCGA 25
Db 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 12
US-08-752-447-1/c
; Sequence 1, Application US/08752447
; Patent No. 5994088
; GENERAL INFORMATION:
; APPLICANT: Mechtner, Eugene
; TITLE OF INVENTION: Method and Reagents for Preparing and
; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenken Hulbert & Berghoff Ltd.
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,447
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5994088nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 95,1121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001

;; TELEFAX: 312-913-9808
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4669 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: 5'UTR
;; LOCATION: 1..424
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 425..4264
;; FEATURE:
;; NAME/KEY: 3'UTR
;; LOCATION: 4265..4669
;; US-08-752-447-1

Query Match 100.0%; Score 25; DB 2; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGAACGAGGCGACGTGCATGGCGA 25
Db 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 13
US-09-316-167-1/c
; Sequence 1, Application US/09316167
; Patent No. 6365357
; GENERAL INFORMATION:
; APPLICANT: Mechtner, Eugene
; APPLICANT: Robinson, Igor B
; TITLE OF INVENTION: Method and Reagents for Preparing and
; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boenken Hulbert & Berghoff Ltd.
; STREET: 300 South Wacker Drive, Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/316,167
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/752,447
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6365357nan, Kevin E
; REGISTRATION NUMBER: 35,303
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 312-913-9808
; TELEPHONE: 312-913-0001
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4669 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: 5'UTR

LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-09-316-167-1

Query Match 100.0%; Score 25; DB 3; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.09; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
Db 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 14
US-09-397-233-1/c
Sequence 1, Application US/09397233
Patent No. 6630327
GENERAL INFORMATION:
APPLICANT: Mechtner, Eugene
Rininson, Igor B
TITLE OF INVENTION: Method and Reagents for Preparing and
Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McDonnell Boehrnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,233
FILING DATE: 16-Sep-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6630327nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-397-233-1

Query Match 100.0%; Score 25; DB 4; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.09; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
Db 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 15
5206352-3/c
Patent No. 5206352
APPLICANT: Rininson, Igor B.; Paetan Ira H.; Gottesman,
Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO: 3
LENGTH: 4669
5206352-3

Query Match 100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.09; 0; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
Db 2064 CGAACGAGGCGACGTGCATGGCGA 2040

Search completed: February 9, 2005, 17:11:19
Job time : 79.592 secs

GenCore version 5.1.6
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OW nucleic - nucleic search, using SW model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds
(without alignments)
602.360 Million cell updates/sec

Title: US-10-007-255-14

Perfect score: 25
Sequence: 1 CGAACCAAGGACGCTGCATGCGCA 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*
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2: geneeqn19908:*
3: geneeqn20008:*
4: geneeqn20018:*
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7: geneeqn20028:*
8: geneeqn20038:*
9: geneeqn20038:*
10: geneeqn20038:*
11: geneeqn20038:*
12: geneeqn20048:*
13: geneeqn20048:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	25	6 AAD39013	Aad39013 Human mdr
C 2	25	100.0	25	6 AAD39003	Aad39003 Human mdr
C 3	25	100.0	2307	6 ABS65230	Abse65230 cDNA enco
C 4	25	100.0	2726	2 AAO70907	Aag70907 Multidrug
C 5	25	100.0	2726	2 AAO70916	Aag70916 Multidrug
C 6	25	100.0	2726	2 AAT43322	Aat43322 Multidrug
C 7	25	100.0	3837	12 ADH22602	Adh22602 cDNA enco
C 8	25	100.0	3840	6 ABV78146	Abv78146 Human mdr
C 9	25	100.0	3840	6 ABZ35722	Abz35722 Human mdr
C 10	25	100.0	3840	6 ABX09965	Abx09965 Human mdr
C 11	25	100.0	3840	6 ABX19687	Abx19687 Human pol
C 12	25	100.0	3843	6 ABQ78185	Abq78185 Human MDR
C 13	25	100.0	3852	8 ABT14496	Abt14496 Rhesus mo
C 14	25	100.0	3858	12 ADH22599	Adh22599 cDNA enco
C 15	25	100.0	3860	3 AAZ49332	Aaz49332 Human wll
C 16	25	100.0	3860	3 AAZ49333	Aaz49333 Human G18
C 17	25	100.0	3860	6 ABA94365	Aba94365 Human BCR
C 18	25	100.0	3860	6 ABA94366	Aba94366 Human BCR
C 19	25	100.0	3924	3 AAZ94742	Aaz94742 Human ATP
C 20	25	100.0	3924	3 AAZ88974	Aaz88974 Human MDR

C 21	25	100.0	3924	6 ABN95801	Abn95801 Gene #229
C 22	25	100.0	3924	11 ADI31842	Adi31842 Human CDN
C 23	25	100.0	3988	3 AAZ88973	Aaz88973 Human MDR
C 24	25	100.0	4039	13 ACN43502	Acn43502 Human dia
C 25	25	100.0	4043	13 ACN41836	Acn41836 Human dia
C 26	25	100.0	4148	13 ACN41835	Acn41835 Human dia
C 27	25	100.0	4186	4 AAF86127	Aaf86127 Cynomolog
C 28	25	100.0	4195	4 AAF86128	Aaf86128 Cynomolog
C 29	25	100.0	4264	2 AAV66533	Aav66533 Mutated h
C 30	25	100.0	4264	2 AAV66534	Aav66534 Mutated h
C 31	25	100.0	4349	2 AAH57442	Aah57442 Human int
C 32	25	100.0	4378	2 AAQ04522	Aaq04522 Multidrug
C 33	25	100.0	4533	6 ABS65229	Abs65229 cDNA enco
C 34	25	100.0	4643	6 ABS76368	Abst76368 cDNA enco
C 35	25	100.0	4643	6 ABV94267	Abv94267 Breast ca
C 36	25	100.0	4643	6 ABV74349	Abv74349 Human ABC
C 37	25	100.0	4643	10 ABX77217	Abx77217 cDNA enco
C 38	25	100.0	4643	12 ADP18689	Adp18689 Human MDR
C 39	25	100.0	4643	12 ADP19748	Adp19748 Human PRO
C 40	25	100.0	4643	13 ADP54881	Adp54881 Human PRO
C 41	25	100.0	4646	2 AAO72872	Aao72872 Human mul
C 42	25	100.0	4646	3 AAQ94738	Aaq94738 Human ATP
C 43	25	100.0	4646	6 ABL68592	Abi68592 Kidney ca
C 44	25	100.0	4646	6 ABL68880	Abi68880 Kidney ca
C 45	25	100.0	4646	6 AAD38994	Aad38994 Human mdr

ALIGNMENTS

RESULT 1
AAD39013/c
ID AAD39013 standard; DNA; 25 BP.

AAD39013;
23-SEP-2002 (first entry)

Human mdr1 gene HIF-1 binding site DNA #6.

Human; haematologic malignancy; multidrug resistance; MDR; SMO-1;
hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;
lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
myeloid disorder; lymphocytic leukemia; thrombocythaemia; myeloma;
angioleitic myeloid metaplasia; myeloid leukemia; gene therapy;
polycythaemia vera; hypoxia responsive element; HRE; ds.

OS Homo sapiens.

Key Location/Qualifiers
misc_binding 11..15
FT /*tag= a
FT /bound_molecule= "HIF-1"

WO200234291-A2.

02-MAY-2002.

25-OCT-2001; 2001WO-US049856.

26-OCT-2000; 2000US-0243542P.

(BGHM) BRIGHAM & WOMENS HOSPITAL INC.

Colgan SP;

WPI; 2002-471427/50.

Treating a subject (at risk of) having a hematologic malignancy or
multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia
inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
binding molecules.

PS Example 2; Page 12; 92pp; English.

XX
CC The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angiosenic
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is human mdrl
CC gene HIF-1 binding site DNA

SO Sequence 25 BP; 2 A; 9 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGCGACGTGCATGCGCA 25
DB 25 CGAACCGGCGACGTGCATGCGCA 1

RESULT 2
AAD39003 standard; DNA; 25 BP.

AC AAD39003;
DT 23-SEP-2002 (first entry)

DE Human mdrl-HRE antisense oligonucleotide #6.

XX
KW Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;
KW hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;
KW lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
KW myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;
KW angiosenic myeloid metaplasia; myeloid leukaemia; gene therapy;
KW polycythaemia vera; hypoxia responsive element; HRE; antisense;
KW phosphorothioate backbone; ss.

XX
OS Homo sapiens.
OS Synthetic.

XX
FH Key Location/Qualifiers
FT modified_base 1..25
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"

XX
WO200234291-A2.

XX
PD 02-MAY-2002.

XX
PF 25-OCT-2001; 2001WO-US049856.

XX
PR 26-OCT-2000; 2000US-0243542P.

XX
PA (BGM) BRIGHAM & WOMENS HOSPITAL INC.

XX
PI Colgan SP;
XX
WIPI; 2002-471427/50.

PT Treating a subject (at risk of) having a hematologic malignancy or
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia
PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

PT binding molecules.

XX
XX Claim 14; Page 43; 92pp; English.

XX
CC The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angiosenic
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is an antisense
CC oligo targeted to HRE in the mdrl gene (mdrl-HRE) to inhibit its
CC expression. This oligo is used in the exemplification of the invention

SO Sequence 25 BP; 7 A; 7 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGCGACGTGCATGCGCA 25
DB 1 CGAACCGGCGACGTGCATGCGCA 25

RESULT 3
ABS65230/C
ID ABS65230 standard; cDNA; 2307 BP.

AC ABS65230;
DT 15-NOV-2002 (first entry)

DE cDNA encoding tumour involved gene (TIG) splice variant, NW-31.

XX
KW Human; ss; gene; splice variant; tumour-involved gene; TIG;
KW pharmaceutical composition; cancer; diagnostic; tumour; gene therapy;
KW endothelial cell; cell differentiation; cell proliferation; apoptosis;
KW gene therapy.

XX
OS Homo sapiens.

XX
PN US2002086384-A1.

XX
PD 04-JUL-2002.

XX
PF 13-MAR-2001; 2001US-00805020.

XX
PR 14-MAR-2000; 2000IL-00135402.
PR 16-MAY-2000; 2000IL-00136154.

XX
PA (LEVI/) LEVINE Z.
PA (DAVI/) DAVID A.
PA (ROMA/) ROMANO C.
PA (BERN/) BERNSTEIN J.

XX
PI Levine Z, David A, Romano C, Bernstein J;
XX
WIPI; 2002-635679/68.
XX
P-PSDB; ABG79700.

PT Novel nucleic acid sequence, which is an alternative splicing variant of
PT tumor involved genes, useful for detecting cancer, predisposition to
PT cancer, for evaluating cancer state and in gene therapy for treating
PT cancer.

PS Claim 1; Page 60-61; 180pp; English.

XX The invention discloses isolated human nucleic acid alternative splicing
CC variants that are all tumour-involved genes (TIGs). The nucleic acids and
CC polypeptides are useful for determining the level of a nucleic acid or
CC polypeptide in a biological sample, for detecting a variant nucleic acid
CC or polypeptide sequence in a biological sample, for determining the level
CC of variant nucleic acid or polypeptide sequences in a biological sample
CC and for determining the ratio between the level of variant sequence in a
CC first biological sample and the level of the original sequence from which
CC the variant has been varied by alternative splicing in a second
CC biological sample and for raising antibodies. A pharmaceutical
CC composition comprising a carrier and the nucleic acid, is useful for
CC treating diseases (e.g. cancer) that can be ameliorated or cured by
CC increasing or decreasing the level of the encoded protein. The nucleic
CC acids are also useful for diagnostic purposes, especially for detecting
CC cancer or a predisposition to cancer, for evaluating the state or
CC aggressiveness of cancer disease, in basic research, for understanding
CC the physiological function of the original TIG, in targeting or
CC developing pharmaceuticals, for distinguishing various stages in the life
CC cycle of the same type of cells which may be helpful for the development
CC of pharmaceuticals for various cancer stages in which cell cycle is non-
CC normal, for determining mutations in tumour-involved genes and in gene
CC therapy. The polypeptides are useful for identifying compounds capable of
CC binding to the variant product and modulating its activity and for
CC modulating endothelial differentiation and proliferation, as well as to
CC modulate apoptosis either ex vivo or in vivo. The sequences presented in
CC AB5652200-AB565235 are the coding sequences for the new variants (NV) 1-
CC 36 of the TIGs disclosed

XX Sequence 2307 BP; 662 A; 441 C; 591 G; 612 T; 0 U; 1 Other;

XX Query Match 100.0%; Score 25; DB 6; Length 2307;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGCGACGTGCAATGGCGA 25

DB 2064 CGAACCGGCGACGTGCAATGGCGA 2040

RESULT 4
AAQ70907/c

ID AAQ70907 standard; DNA; 2726 BP.

XX AAQ70907;

AC 25-MAR-2003 (revised)

DT 27-MAR-1995 (first entry)

XX Multidrug-resistance gene MDR-1.

XX Multidrug-resistance; MDR-1 gene; ds.

XX Synthetic.

XX WO9417206-A1

XX 04-AUG-1994.

XX 12-NOV-1993; 93WO-US010883.

XX 27-JAN-1993; 93US-00010433.

XX (ONCO-) ONCOR INC.

XX Bhatnagar SK, George AL;

XX WPI; 1994-264118/32.

PT Enzymatic amplification of target nucleic acid sequences in a mixt. - to
PT detect a mutation or allele in the target, e.g. that causes a genetic
PT disease.

XX Disclosure; Page 30; 50pp; English.

XX This gene is used as an example of a target DNA in a method for the
CC amplification of nucleic acid sequences in a mixture using various DNA
CC probes/primers. The method may be used to detect a mutation or allele in
CC the target, e.g. that causes a genetic disease; (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 2; Length 2726;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGCGACGTGCAATGGCGA 25

DB 144 CGAACCGGCGACGTGCAATGGCGA 120

RESULT 5

AAQ70916/c

ID AAQ70916 standard; DNA; 2726 BP.

XX AAQ70916;

AC 25-MAR-2003 (revised)

DT 27-MAR-1995 (first entry)

XX Multidrug-resistance gene MDR-1.

XX Multidrug-resistance; MDR-1 gene; ds.

XX Synthetic.

XX WO9417210-A1.

XX 04-AUG-1994.

XX 25-JAN-1994; 94WO-US000748.

XX 27-JAN-1993; 93US-00010433.

XX 16-DEC-1993; 93US-00168621.

XX (ONCO-) ONCOR INC.

XX Bhatnagar SK, George AL;

XX WPI; 1994-264122/32.

XX Disclosure; Page 30; 69pp; English.

XX This gene is used as an example of a target DNA in a method for the
CC amplification of nucleic acid sequences in a mixture using various DNA
CC probes/primers. The method may be used to detect a mutation or allele in
CC the target, e.g. that causes a genetic disease; (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 2; Length 2726;

XX Best Local Similarity 100.0%; Pred. No. 0.14;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGCGACGTGCAATGGCGA 25

DB 144 CGAACCGGCGACGTGCAATGGCGA 120

RESULT 6
AAT43322/c
ID AAT43322 standard; DNA; 2726 BP.
XX
AC AAT43322;
XX
AT 01-SEP-1997 (first entry)
XX
DE Multidrug resistance gene-1.
XX
KM PCR primer; amplify; polymerase chain reaction; ligase chain reaction;
XX LCR; human; multidrug resistance gene; MDR-1; ds.
XX
OS Synthetic.
XX
PM WO9639537-A1.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-US008841.
XX
PR 05-JUN-1995; 95US-00461823.
XX
PA (ONCO-) ONCOR INC.
XX
PI Bhatnagar SK, George AL, Nazarenko I;
XX WPI; 1997-043158/04.
XX
PT Amplification method avoiding strand displacement by polymerase - used in
PT the detection of mutation(s) and allele(s) associated with genetic
PT disease and cancer.
XX
PS Example 1; Page 50-51; 92pp; English.
XX
CC This sequence represents the multidrug resistance gene (MDR-1) amplified
CC by the primers shown in AAT43320 and AAT43321. This sequence can be used
CC as a target in the method of the invention, for enzymatically amplifying
CC a target nucleic acid (TNA) sequence contained in a nucleic acid or
CC mixture of nucleic acids while avoiding strand displacement by
CC polymerase. The method comprises using three primers, one complementary
CC to a first segment of the TNA, a second complementary to a second segment
CC of the TNA, which is adjacent to the first primer, and a third which is
CC similar to the first primer. The first two primers are hybridised to a
CC portion of the first primer. The first two primers are hybridised to the
CC TNA, and a fused amplification product is created from the TNA using
CC these two primers. The fused product is dissociated, and hybridised to
CC the third primer, which is then extended. The extended modified
CC amplification product is hybridised to the first two primers, and these
CC two primers are ligated. Each of the primers may be labelled using a
CC different label so that the method can be used to detect the presence of
CC a mutation or allele by detecting whether the labelled primer is
CC contained within the fused amplification product or the extended
CC amplification product. The method of the invention combines certain
CC aspects of ligase chain reaction (LCR) and polymerase chain reaction
CC (PCR), but is improved compared to LCR due to the reduced number of
CC primers needed, and the fact that the entire TNA sequence does not need
CC to be known
XX
SQ Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 2726;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCAGGGCAGCTGCATGGCGA 25
|||||
Db 144 CGAACGAGGGCAGCTGCATGGCGA 120
|||||

RESULT 7
ADH22602/c
ID ADH22602 standard; cDNA; 3837 BP.

XX
AC ADH22602;
XX
AT 11-MAR-2004 (first entry)
XX
DE cDNA encoding a human transporter & ion channel (TRICH) protein SeqID100.
XX
KM gene; ss; human; transporters and ion channel; TRICH; cell proliferative;
XX arteriosclerosis; cancer; autoimmune/inflammatory; AIDS; asthma;
XX neurological; epilepsy; stroke; developmental; Cushing's syndrome;
XX hypothyroidism; infection; gene therapy; cytostatic; antiinflammatory;
XX immunosuppressive; antiaesthetic; anticonvulsant; nootropic;
XX neuroprotective.
XX
OS Homo sapiens.
XX
PM WO2003093444-A2.
XX
PD 13-NOV-2003.
XX
PF 02-MAY-2003; 2003WO-US014026.
XX
PR 03-MAY-2002; 2002US-0377435P.
XX
PR 03-MAY-2002; 2002US-0377444P.
XX
PR 05-JUN-2002; 2002US-0386497P.
XX
PR 11-JUN-2002; 2002US-0388180P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Baughn MR, Becha SD, Bulloch SA, Chang H, Elliott VS;
XX Emerling BM, Griffin JA, Hafalia AJA, Ison CH, Jackson AA, Jiang X;
XX Jin P, Kable AE, Khare R, Lee SY, Lee S, Mason PM, Margulis JP;
XX Ramkumar J, Richardson TW, Swarnakar A, Tran UK, Chawla NK;
XX Wilson AD;
XX WPI; 2004-022655/02.
XX
DR P-PSDB; ADH22536.
XX
PT New human transporters and ion channels (TRICH), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant TRICH expression e.g. cancer, AIDS, arteriosclerosis, epilepsy,
PT or infections.
XX
PS Claim 12; SEQ ID NO 100; 448bp; English.
XX
CC This invention relates to novel isolated polynucleotides identified as
CC human transporters and ion channels (TRICH), and the encoded polypeptides
CC thereof. Specifically, it describes using these TRICH molecules, as well
CC as agonists, antagonists, antibodies, expression vectors and host cells,
CC in appropriate screening and toxicity assays to assess the effects of
CC exogenous compounds on TRICH expression. The present invention describes
CC TRICH compositions that are useful in the diagnosis, treatment and
CC prevention of various disorders such as cell proliferative (e.g.
CC arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma),
CC neurological (e.g. epilepsy, stroke) and developmental (e.g. Cushing's
CC syndrome hypothyroidism) and for infections. Accordingly, these TRICH
CC molecules can be used for gene therapy purposes and exhibit various
CC activities such as cytostatic, antiinflammatory, immunosuppressive,
CC antiaesthetic, anticonvulsant, nootropic and neuroprotective.
CC Furthermore, a microarray is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions and gene expression
CC profiles. This polynucleotide sequence is a human TRICH cDNA of the
CC invention.
XX
SQ Sequence 3837 BP; 1130 A; 772 C; 962 G; 973 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 3837;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGGCAGCTGCATGGCGA 25
|||||
Db 1675 CGAACGAGGGCAGCTGCATGGCGA 1651
|||||

RESULT 8
ABV78146/c
ID ABV78146 standard; DNA; 3840 BP.
XX
AC ABV78146;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human mdr-1 DNA SEQ ID NO 30.
XX
KM RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;
KM virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200255693-A2.
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
PI Kreutzler R, Limmer S, Roet S, Hadwiger P;
DR WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
PS Claim 10; Page 131-132; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (asi) of dsRNA is complementary to (I) and at least one end of dsRNA
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGGCAGTCGCAATGGCGA 25
DB 1637 CGAACCGGGCAGTCGCAATGGCGA 1613

RESULT 9
ABZ35722/c
ID ABZ35722 standard; DNA; 3840 BP.
XX
AC ABZ35722;
XX
DT 07-FEB-2003 (first entry)
XX
DE Human mdr-1 polynucleotide SEQ ID NO 30.

XX Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KM protozoacide; gene expression; antisense; tumour; infection; plasmodium;
KM virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KM Hepatitis C virus; human papilloma virus; gene; ds.
XX
OS Homo sapiens.
XX
PN DE10100588-A1.
PD 18-JUL-2002.
XX
PF 09-JAN-2001; 2001DE-01000588.
XX
PR 09-JAN-2001; 2001DE-01000588.
XX
PA (RIBO-) RIBOPHARMA AG.
PI Kreutzler R, Limmer S, Roet S, Hadwiger P;
DR WPI; 2002-683450/74.
XX
PF Inhibiting expression of target genes, useful e.g. for treating tumour,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.
XX
PS Claim 13; Page 27-28; 100pp; German.
XX
CC The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligoribonucleotides (dsRNAI and II), both
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNAI and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expressions than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
XX
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGGGCAGTCGCAATGGCGA 25
DB 1637 CGAACCGGGCAGTCGCAATGGCGA 1613

RESULT 10
ABX09965/c
ID ABX09965 standard; DNA; 3840 BP.
XX
AC ABX09965;
XX
DT 23-JAN-2003 (first entry)
XX
DE Human mdr-1 DNA fragment SEQ ID 30.
XX
KM Oligoribonucleotide; interferon; oncogene; cytokine; id; developmental;
KM prion; inhibition; human; ds.
XX
OS Homo sapiens.
XX
PN DE10100587-C1.
PD 21-NOV-2002.
XX

PF 09-JAN-2001; 2001DE-01000587.
XX
PR 09-JAN-2001; 2001DE-01000587.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzner R, Limmer S, Roest S, Hadwiger P;
DR WPI; 2002-742209/81.
XX
PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by
PT introduction of complementary double-stranded oligoribonucleotide, after
PT treating the cell with interferon.
XX
PS Disclosure; Page 32-33; 98pp; German.
XX
CC This invention describes a novel method for inhibiting expression of a
CC target gene by introducing into the cell that contains the target gene at
CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
CC structure of not more than 49 consecutive nucleotides (nt), where at
CC least a segment of one strand of the ds structure is complementary with
CC the target gene and the cells are treated with interferon before
CC introduction of dsRNA. The method is used to inhibit expression of
CC target genes, particularly oncogenes, cytokine genes, Id (not defined)
CC protein genes; developmental or prion genes, or genes expressed in
CC pathogenic organisms (particularly plasmodia) or in viruses or viroids
CC (pathogenic in humans, animals or plants). Treating the cells with
CC interferon greatly increases the extent to which dsRNA can inhibit
CC expression of the target genes, and the effect is even greater when dsRNA
CC are modified to increase their stability. ABX09936-ABX10075 represent
CC gene fragments used to illustrate the method of the invention
XX
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGAACCGGGCAGCTGCAATGGCGA 25
Db 1637 CGAACCGGGCAGCTGCAATGGCGA 1613
RESULT 11
ABL91687/C
ID ABL91687 standard; DNA; 3840 BP.
XX
AC ABL91687;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 30.
XX
KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KW cytostatic; virucide; protozoacide; antibacterial; ds.
XX
OS Homo sapiens.
XX
PN DE10100586-C1.
XX
PD 11-APR-2002.
XX
PF 09-JAN-2001; 2001DE-01000586.
XX
PR 09-JAN-2001; 2001DE-01000586.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzner R, Limmer S, Roest S, Hadwiger P;
DR WPI; 2002-270454/32.
XX

PT Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT introducing double-stranded complementary oligoRNA having unpaired
PT terminal bases.
XX
XX Claim 13; Page 28-30; 104pp; German.
XX
PS The invention relates to a method for inhibiting expression of a target
CC gene (ABL91658-ABL91797) in a cell by introducing at least one
CC oligoribonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one end a single-
CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC antisense inhibition of gene expression useful e.g. for treating tumors
CC but the oligoribonucleotides may also be directed against genes present
CC in pathogens (e.g. Plasmodium or viruses/viroids; pathogenic on humans,
CC animals or plants) or against cytokine, Id, developmental or prion genes.
CC The method provides more effective inhibition of gene expression than use
CC of known oligonucleotides, probably because the unpaired overhang
CC increases stability and thus intracellular concentration
XX
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGAACCGGGCAGCTGCAATGGCGA 25
Db 1637 CGAACCGGGCAGCTGCAATGGCGA 1613
RESULT 12
ABQ78185/C
ID ABQ78185 standard; cDNA; 3843 BP.
XX
AC ABQ78185;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human MDR1 encoding cDNA SEQ ID NO 1.
XX
KW Human; immunosuppressant; tacrolimus; cyclosporin; MDR1; SNP;
KW single nucleotide polymorphism; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3843
FT /*tag= a
FT /product= "MDR1"
FT replace(2677,A/T)
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
XX
PN JP2002223769-A.
XX
PD 13-AUG-2002.
XX
PF 31-JAN-2001; 2001JP-00024723.
XX
PR 31-JAN-2001; 2001JP-00024723.
XX
PA (SRLS-) SRL KK.
XX
XX WPI; 2002-639348/69.
DR P-PSDB; ABB83950.
XX
PT Presuming the side effect of an immunosuppressant comprises using a
PT primer set.
XX
PS Disclosure; Page 6-11; 14pp; Japanese.
XX
CC The invention relates to presumption of the side effect of at least one

QY 1 CGAAC CAGGG CACGT GCAAT GGGCA 25
Db 1675 CGAAC CAGGG CACGT GCAAT GGGCA 1651

RESULT 15
AAZ49332/c
ID AAZ49332 standard; cDNA; 3860 BP.

AC AAZ49332;

DT 14-MAR-2000 (first entry)

Human wild-type multidrug resistance-1 (MDR-1) cDNA.

KW Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;
 KW haematopoietic stem cell; transplantation; bone marrow transplantation;
 KW chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;
 KW genetic defect; thalassaemia; Gaucher's disease; sickle cell anaemia;
 KW leukaemia; ex vivo expansion; cytokine; wild-type; ds.

OS Homo sapiens.

FH	Key	Location/Qualifiers

FT	CDS	1.	.3843
----	-----	----	-------

FT / *tag= a

FT mutation replace(553..555, GTT)

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FT /notes= "CDNA sequence of G185V human mutant MDR-1 given
PT in AAZ49333"
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PN W09961589-A2.

PD 02-DEC-1999

PF 27-MAY-1999; 99WO-US011825.

PR 28-MAY-1998; 98US-0086988P.

PA (SUJD-) ST JUDE CHILDREN'S RES HOSPITAL.

PI Sorrentino B, Bunting K;

DR WPI; 2000-072615/06.

DR P-PSDB; AAY58186.

PT Ex vivo expansion of hematopoietic stem cells transduced with a sequence encoding human multidrug resistance-1, used for bone marrow transplantation.

PS Claim 10; Page 68-70; 113pp; English.

This sequence represents cDNA encoding human wild-type multidrug resistance protein MDR-1. MDR-1 is a transmembrane efflux pump. CC responsible for the export of drugs from cells, particularly cancer CC cells. Wild-type MDR-1 shows increased resistance to etoposide and CC decreased resistance to vinca alkaloids compared with a mutant form CC (MAY58187) where the Gly at position 185 is replaced by Val. The CC invention relates to transducing haematopoietic stem cells with nucleic CC acid encoding an MDR protein and culturing the modified cells. The CC modified haematopoietic stem cells are useful in bone marrow CC transplantation (to reconstitute haematopoietic systems in patients who CC have undergone chemotherapy or radiation therapy) and in ex vivo gene CC therapy of genetic defects in cells derived from haematopoietic stem CC cells, e.g., thalassemia, Gaucher's disease, sickle cell anaemia or CC leukaemia. The modified cells can also be used to identify factors CC involved in regulating proliferation and differentiation in CC haematopoietic stem cells. Haematopoietic stem cells that express MDR-1 CC will be protected against chemotherapeutic agents, so can be engineered CC while the patient is undergoing chemotherapy. Expansion of (rare) CC haematopoietic stem cells provides sufficient cells to permit standard CC biochemical analysis. Overexpression of MDR-1 allows cytokine-driven

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OM nucleic - nucleic search, using SW model

Run on: February 9, 2005, 13:42:02; Search time 266.667 Seconds
(without alignments)
539.601 Million cell updates/sec

Title: US-10-007-255-14

Perfect score: 25
Sequence: 1 CGAACCGAGGCGACGTGCATGCGCA 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	100.0	2307	9	US-09-805-020-31	Sequence 31, Appl
2	100.0	3825	17	US-10-363-112-48	Sequence 48, Appl
3	100.0	3840	18	US-10-384-339C-30	Sequence 30, Appl
4	100.0	3852	15	US-10-101-433A-1	Sequence 1, Appl
5	100.0	3860	9	US-09-866-866A-3	Sequence 1, Appl
6	100.0	3860	9	US-09-866-866A-3	Sequence 3, Appl
7	100.0	3924	17	US-09-880-107-2299	Sequence 2299, Ap
8	100.0	3924	17	US-10-641-643-1168	Sequence 1168, Ap
9	100.0	4186	17	US-10-619-359A-1	Sequence 1, Appl
10	100.0	4195	17	US-10-619-359A-3	Sequence 3, Appl
11	100.0	4533	9	US-09-805-020-30	Sequence 30, Appl

12	25	100.0	4643	13	US-10-072-621-2	Sequence 2, Appl
13	25	100.0	4643	15	US-10-097-340-1	Sequence 1, Appl
14	25	100.0	4643	14	US-10-007-925A-258	Sequence 258, App
15	25	100.0	4646	11	US-09-968-007A-459	Sequence 459, App
16	25	100.0	4646	11	US-09-968-007A-747	Sequence 747, App
17	25	100.0	4646	17	US-10-641-643-1167	Sequence 1167, App
18	25	100.0	4646	17	US-10-343-657-1	Sequence 1, Appl
19	25	100.0	4646	18	US-10-775-169-198	Sequence 198, App
20	25	100.0	4669	18	US-10-680-516-1	Sequence 1, Appl
21	25	100.0	8630	9	US-09-306-417-2	Sequence 1, Appl
22	25	100.0	8630	9	US-09-306-417-2	Sequence 2, Appl
23	21.8	87.2	4317	13	US-10-044-671-1	Sequence 1, Appl
24	21.8	87.2	4317	18	US-10-896-434-1	Sequence 1, Appl
25	20.2	80.8	3912	9	US-09-917-800A-1560	Sequence 1560, Ap
26	20.2	80.8	4189	9	US-09-866-866A-5	Sequence 5, Appl
27	20.2	80.8	4254	9	US-09-917-800A-1424	Sequence 1424, Ap
28	20.2	80.8	4254	17	US-10-388-934-265	Sequence 265, App
29	20.2	80.8	4254	17	US-10-388-934-265	Sequence 1484, Ap
30	20.2	80.8	4298	18	US-10-152-319A-1484	Sequence 32, Appl
31	20.2	80.8	4369	9	US-10-335-053-32	Sequence 1, Appl
32	20.2	80.8	4425	9	US-09-769-097-3	Sequence 7, Appl
33	20.2	80.8	4788	9	US-09-866-866A-7	Sequence 3184, A
34	19.2	76.8	711	17	US-10-369-493-3184	Sequence 4149, A
35	19.2	76.8	747	17	US-10-369-493-31419	Sequence 59, Appl
36	19.2	76.8	7615	16	US-10-004-113-59	Sequence 4, Appl
37	19.2	76.8	55001	17	US-10-160-497-4	Sequence 4, Appl
38	19.2	76.8	55001	17	US-10-348-750-4	Sequence 1, Appl
39	19.2	76.8	2731748	18	US-10-297-465A-1	Sequence 38, Appl
40	19	76.0	19	17	US-10-016-490C-38	Sequence 29889, A
41	18.8	75.2	483	17	US-10-369-493-29889	Sequence 11, Appl
42	18.6	74.4	1175	15	US-09-873-409-11	Sequence 2443, Ap
43	18.6	74.4	1818	9	US-10-156-761-2443	Sequence 16, Appl
44	18.6	74.4	1940	9	US-09-873-409-15	Sequence 15, Appl
45	18.6	74.4	2021	9	US-09-873-409-15	

ALIGNMENTS

RESULT 1
US-09-805-020-31/c
Sequence 31, Application US/09805020
Publication No. US20020086384A1
GENERAL INFORMATION:
APPLICANT: LEVINE, Zurit
TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
FILE REFERENCE: 2786-0168P
CURRENT APPLICATION NUMBER: US/09/805,020
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 2307
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(2307)
OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-31

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Best Local Similarity 100.0%; Pred. No. 0.034; Mismatches 0; Indels 0; Gaps 0;
Matches 25; Conservative 0;

QY 1 CGAACCGAGGCGACGTGCATGCGCA 25
DB 2064 CGAACCGAGGCGACGTGCATGCGCA 2040

RESULT 2
US-10-363-112-48/c
Sequence 48, Application US/10363112

Publication No. US20040091964A1
GENERAL INFORMATION:
APPLICANT: THE AUSTRALIAN NATIONAL UNIVERSITY
APPLICANT: BOARD, PHILIP
APPLICANT: HARRIS, MATTHEW
TITLE OF INVENTION: MODIFIED PROTEINS, ISOLATED NOVEL PEPTIDES, AND USES THEREOF
FILE REFERENCE: 007643-0302189
CURRENT APPLICATION NUMBER: US/10/363,112
CURRENT FILING DATE: 2003-11-03
PRIOR APPLICATION NUMBER: PCT/AU01/01093
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/229,663
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 3825
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3825)
US-10-363-112-48

Query Match 100.0%; Score 25; DB 17; Length 3825;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1646 CGAACGAGGCGACGTGCAATGGCGA 1622

RESULT 3
US-10-384-339C-30/C
Sequence 30, Application US/10384339C
Publication No. US20040175703A1
GENERAL INFORMATION:
APPLICANT: Kreutzer, Roland
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
FILE REFERENCE: 20200/2002
CURRENT APPLICATION NUMBER: US/10/384,339C
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: DE 10100586.5
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 3840
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
TITLE: mdr-1
PATENT DOCUMENT NUMBER: AF016535
US-10-384-339C-30

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Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-101-433A-1/C
Sequence 1, Application US/10101433A
Publication No. US20030119726A1
GENERAL INFORMATION:
APPLICANT: Hanacom, Sara
APPLICANT: Crespi, Charles
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G00307/70019
CURRENT APPLICATION NUMBER: US/10/101,433A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/277,095
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3852
TYPE: DNA
ORGANISM: Macaca mulatta
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3852)
US-10-101-433A-1

Query Match 100.0%; Score 25; DB 15; Length 3852;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCAATGGCGA 25
DB 1649 CGAACGAGGCGACGTGCAATGGCGA 1625

RESULT 5
US-09-866-866A-1/C
Sequence 1, Application US/09866866A
Patent No. US20020102244A1
GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3860
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-866A-1

Query Match 100.0%; Score 25; DB 9; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGAACGAGGCGACGTGCAATGGCGA 25
DB 1640 CGAACGAGGCGACGTGCAATGGCGA 1616

RESULT 6
US-09-866-866A-3/C
Sequence 3, Application US/09866866A
Patent No. US20020102244A1
GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian

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; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-866-866A-3

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Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCAGGCGACGTGCAATGGCGA 25
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Db 1640 CGAACCAGGCGACGTGCAATGGCGA 1616

RESULT 7
US-09-880-107-2239/c
; Sequence 2239, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2299
; LENGTH: 3924
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M23234
; US-09-880-107-2239

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Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCAGGCGACGTGCAATGGCGA 25
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Db 1678 CGAACCAGGCGACGTGCAATGGCGA 1654

RESULT 8
US-10-641-643-1168/c
; Sequence 1168, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cooke, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
```

```

; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; CITY: PALO ALTO
; STREET: 3174 PORTER DRIVE
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g187501
; SEQUENCE DESCRIPTION: SEQ ID NO: 1168 :
US-10-641-643-1168

Query Match          100.0%; Score 25; DB 17; Length 3924;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCAGGCGACGTGCAATGGCGA 25
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Db 1678 CGAACCAGGCGACGTGCAATGGCGA 1654

RESULT 9
US-10-619-359A-1/c
; Sequence 1, Application US/10619359A
; Publication No. US20040077000A1
; GENERAL INFORMATION:
; APPLICANT: STOCKER, PENNY J.
; APPLICANT: STEIMEL-CRESPI, DOROTHY T.
; APPLICANT: CRESPI, CHARLES L.
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307.70020.US
; CURRENT APPLICATION NUMBER: US/10/619,359A
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/156,921
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/158,818
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 09/672,810
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 4186
; TYPE: DNA
; ORGANISM: Macaca fascicularis
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FEATURE:
NAME/KEY: CDS
LOCATION: (100)...(3940)
US-10-619-359A-1

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Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 1739 CGAACGAGGCGACGTGCATGGCGA 1715

RESULT 10
US-10-619-359A-3/c
Sequence 3, Application US/10619359A
Publication No. US20040077000A1
GENERAL INFORMATION:
APPLICANT: STOCKER, PENNY J.
APPLICANT: STEIMEL-CRESPI, DOROTHY T.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G00307.70020.US
CURRENT APPLICATION NUMBER: US/10/619,359A
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1998-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: US 09/672,810
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 4195
TYPE: DNA
ORGANISM: Macaca fascicularis
FEATURE:
NAME/KEY: CDS
LOCATION: (100)...(3949)
US-10-619-359A-3

Query Match 100.0%; Score 25; DB 17; Length 4195;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 1748 CGAACGAGGCGACGTGCATGGCGA 1724

RESULT 11
US-09-805-020-30/c
Sequence 30, Application US/09805020
Publication No. US20020086384A1
GENERAL INFORMATION:
APPLICANT: LEVINE, Zurit
TITLE OF INVENTION: SPICE VARIANTS OF ONCOGENES
FILE REFERENCE: 2786-0168P
CURRENT APPLICATION NUMBER: US/09/805,020
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 4533
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(4533)
OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-30

Query Match 100.0%; Score 25; DB 9; Length 4533;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 2064 CGAACGAGGCGACGTGCATGGCGA 2040

RESULT 12
US-10-072-621-2/c
Sequence 2, Application US/10072621
Publication No. US20020169137A1
GENERAL INFORMATION:
APPLICANT: Reiner, Peter B.
APPLICANT: Connop, Bruce P.
APPLICANT: Pollard, Michelle
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY
FILE REFERENCE: 100103.402
CURRENT APPLICATION NUMBER: US/10/072,621
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
US-10-072-621-2

Query Match 100.0%; Score 25; DB 13; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCATGGCGA 25
DB 2061 CGAACGAGGCGACGTGCATGGCGA 2037

RESULT 13
US-10-097-340-1/c
Sequence 1, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOBESCH
APPLICANT: Shubhangi KAMATRAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel B. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967


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; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-1

Query Match          100.0%; Score 25; DB 14; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGCAGTGCATGCGCA 25
DB 2061 CGAACGAGGCGCAGTGCATGCGCA 2037

RESULT 14
US-10-007-926A-258/c
; Sequence 258, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOUIGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: PERR, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: atp-binding cassette, sub-family b
; OTHER INFORMATION: (mdr/cap), member 1 (ABCB1) gene.
US-10-007-926A-258

Query Match          100.0%; Score 25; DB 15; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGCAGTGCATGCGCA 25
DB 2061 CGAACGAGGCGCAGTGCATGCGCA 2037

RESULT 15
US-09-968-007A-459/c
; Sequence 459, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Edner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
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; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 459
; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-459

Query Match          100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGCAGTGCATGCGCA 25
DB 2064 CGAACGAGGCGCAGTGCATGCGCA 2040

Search completed: February 9, 2005, 22:26:42
Job time : 268.667 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds
(without alignments)
388.593 Million cell updates/sec

Title: US-10-007-255-14
Perfect score: 25
Sequence: 1 cgaaccaggcagcgtcgaatgcgga 25

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	290	7 F07318	F07318 HSC22A071 n
2	25	100.0	315	7 F08704	F08704 HSC22A021 n
3	25	100.0	320	7 F08211	F08211 HSC22C011 n
4	25	100.0	328	7 F06233	F06233 HSC1E051 n
5	25	100.0	357	7 T26505	T26505 AB282ER1 n
6	25	100.0	469	7 R53330	R53330 Y983B02.r1
7	25	100.0	568	5 BP243819	BP243819 BP243819
8	25	100.0	570	5 BP220580	BP220580 BP220580
9	25	100.0	669	9 AG179058	AG179058 Pan trogl
10	25	100.0	699	9 AG179442	AG179442 Pan trogl
11	25	100.0	3843	9 AY408954	AY408954 Homo sapi
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13	25	100.0	4035	3 BC042531	BC042531 Homo sapi
14	23.4	93.6	680	9 AG179392	AG179392 Pan trogl
15	23.4	93.6	360	1 AV191114	AV191114 AV191114
16	20.2	80.8	360	6 C12346	C12346 C12346 Yui1
17	20.2	80.8	374	1 AA789728	AA789728 vt78c08.r
18	20.2	80.8	485	6 CB727009	CB727009 AMGNRUC.N
19	20.2	80.8	550	4 BJ075336	BJ075336 BU075336
20	20.2	80.8	824	9 CC475658	CC475658 CH240_301
21	20.2	80.8	2792	3 AK050345	AK050345 Mus muscu
22	20.2	80.8	3182	3 AK030328	AK030328 Mus muscu
23	20.2	80.8	3816	9 AY408956	AY408956 Mus muscu
24	19.2	76.8	347	8 BZ840467	BZ840467 CH240_237

25	19.2	76.8	429	7 CF136217	CF136217 UI-HF-BN0
26	19.2	76.8	446	5 BQ343554	BQ343554 RCO-NT003
27	19.2	76.8	569	5 CR241012	CR241012 Reverse s
28	19.2	76.8	578	9 CE805931	CE805931 ligr-gs21
29	19.2	76.8	663	7 CN431062	CN431062 170005321
30	19.2	76.8	726	8 BH112888	BH112888 RPT-24-2
31	19.2	76.8	754	7 CN431066	CN431066 170004245
32	19.2	76.8	845	4 BG818192	BG818192 602779778
33	19.2	76.8	3721	3 BC032414	BC032414 Homo sapi
34	18.8	75.2	392	1 A115290	A115290 uba7h07.r
35	18.8	75.2	380	2 BE687194	BE687194 uv94b10.y
36	18.8	75.2	638	1 AA175587	AA175587 ms95a01.r
37	18.8	75.2	639	7 CFS99341	CFS99341 NCST3d93
38	18.8	75.2	641	4 BJ814960	BJ814960 BJ814960
39	18.8	75.2	656	4 BJ818135	BJ818135 BJ818135
40	18.8	75.2	710	1 AA185993	AA185993 mt35b02.r
41	18.8	75.2	757	5 BU314758	BU314758 603544822
42	18.8	75.2	800	7 BG704400	BG704400 HR04521_B
43	18.8	75.2	859	4 BG704400	BG704400 602687466
44	18.6	74.4	360	6 C67438	C67438 C67438 Yui1
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ALIGNMENTS

RESULT 1	F07318	290 bp	MRNA	linear	EST 20-FEB-1995
LOCUS	HSC22A071	normalized infant brain cDNA	Homo sapiens	CDNA clone	
DEFINITION	C-22A07, mRNA sequence.				
ACCESSION	F07318				
VERSION	F07318.1	GI:672970			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 290)				
AUTHORS	Aufrey, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houligatte, R., Junneau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pletu, G., Poulliot, Y., Sebastiani-Kabakchis, C. and Tessier, A.				
TITLE	IMAGE: molecular integration of the analysis of the human genome and its expression				
JOURNAL	C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)				
MEDLINE	95277534				
PUBMED	7757816				
COMMENT	Contact: Genethon Genethon Centre de recherche sur le Genome Humain 1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE Tel: 33169472800 Fax: 33160778698 Email: genethon@genethon.fr Single read. Genethon library, idt: C, Genethon_sequence_idt: Y1C-22A07 Seq primer: (-21)M13 universal. Location/Qualifiers 1..290 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="C-22A07" /sex="Female" /tissue_type="total brain" /dev_stage="3 months old" /clone_lib="normalized infant brain cDNA" /note="Organ: brain; Vector: lambdaB; Site 1: HindIII; Site 2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the				

lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 290;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGAGGACGTGCATGCGCA 25
DB 243 CGAACCGAGGACGTGCATGCGCA 267

RESULT 2

LOCUS F08704 315 bp mRNA linear EST 21-FEB-1995
DEFINITION HSCZ0A021 normalized infant brain cDNA Homo sapiens CDNA clone
c-zoa02, mRNA sequence.

ACCESSION F08704
VERSION F08704.1 GI:6777708
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 315)
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,
Devignes, M.D., Duprat, S., Houligatte, R., Jumeau, M.N., Lamy, B.,
Lorenzo, F., Mitchell, H., Marriage-Samson, R., Pletu, G., Pouillot, Y.,
Sebastiani-Kabatchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

TITLE

JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534
PubMed 7757816

COMMENT

Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress library_id: C; Genexpress_sequence_id: y2c-zoa02
Seg primer: (-21)M13 universal.
Location/Qualifiers
1..315
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/mol_type="mRNA"
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/sex="Female"
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/dev_stage="3 months old"
/clone_lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;
Site 2: NotI; sex=Female; dev stages=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

FEATURES

source

ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 315;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGAGGACGTGCATGCGCA 25
DB 243 CGAACCGAGGACGTGCATGCGCA 267

RESULT 3

LOCUS F08211 320 bp mRNA linear EST 21-FEB-1995
DEFINITION HSCZ0C011 normalized infant brain cDNA Homo sapiens CDNA clone
c-zoc01, mRNA sequence.

ACCESSION F08211
VERSION F08211.1 GI:677727
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 320)
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,
Devignes, M.D., Duprat, S., Houligatte, R., Jumeau, M.N., Lamy, B.,
Lorenzo, F., Mitchell, H., Marriage-Samson, R., Pletu, G., Pouillot, Y.,
Sebastiani-Kabatchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

TITLE

JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534
PubMed 7757816

COMMENT

Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress library_id: C; Genexpress_sequence_id: y1c-zoc01
Seg primer: (-21)M13 universal.
Location/Qualifiers
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/clone="c-zoc01"
/sex="Female"
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/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;
Site 2: NotI; sex=Female; dev stages=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

FEATURES

source

ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGAACCGAGGACGTGCATGCGCA 25
DB 243 CGAACCGAGGACGTGCATGCGCA 267

RESULT 4

LOCUS F06233 328 bp mRNA linear EST 19-FEB-1995
DEFINITION HSC11E051 normalized infant brain cDNA Homo sapiens CDNA clone
c-11e05, mRNA sequence.

ACCESSION F06233
VERSION F06233.1 GI:670049
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 328)

TITLE

Auffray, C., Behar, G., Bole, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houllgate, R., Juneau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebasteian-Kabackich, C. and Tessier, A. IMAGE: molecular integration of the analysis of the human genome and its expression

JOURNAL

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

MEDLINE
PUBMED

9527534

7757816

COMMENT

Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress library_id: C; Genexpress_sequence_id: y1c-11e05
Seq primer: (-21)M13 universal.

FEATURES

SOURCE

location/Qualifiers

1..328

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="C-11e05"

/sex="Female"

/tissue_type="total brain"

/dev_stage="3 months old"

/clone_lib="normalized infant brain cDNA"

/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;

Site_2: NotI; sex:Female; dev stage=3 months old;

Isolate=muscular atrophy patient; tissue type=total

brain; total mRNA was oligo-(dT) primed and directionally

cloned 5' -> 3' into the HindIII -> NotI sites of the

lafmid BA vector. Clone library from B.Saeres, Psychiatry

Dept. Columbia University, USA. Normalization_method:

Bento Soares, P.N.A.S in press"

ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGAACCAGGCGACGTGCATGGCGA 25

243 CGAACCAGGCGACGTGCATGGCGA 267

RESULT 5

LOCUS T26505 357 bp mRNA linear EST 15-APR-1996

DEFINITION AB282E2R Infant brain, LNL array of Dr. M. Soares INIB Homo

sapiens cDNA clone L1AB282E2 5', mRNA sequence.

ACCESSION T26505

VERSION T26505.1 GI:773822

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 357)

Chico, N.S., Eveleth, G.G., Lieuallen, K. and Lennon, G.G.

Infant brain cDNA

Genomics 28 (3), 570-572 (1995)

96039272

7490096

PUBMED

COMMENT

Contact: Greg G. Lennon
Human Genome Center, L-452
Lawrence Livermore National Laboratory
Livermore CA 94550

FEATURES

SOURCE

Tel: 510 422 8361
Fax: 510 422 2282
Email: info@image.llnl.gov
Seq primer: M13 Reverse.
Location/Qualifiers

1..357

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="L1AB282E2"

/note="Vector: lafmid BA; Site_1: HindIII; Site_2: NotI;

Normalized infant brain cDNA library made by Dr. M. Soares

(Columbia University), oligo-dT primed and directionally

cloned between HindIII (5') and NotI (3') sites "

ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 357;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGAACCAGGCGACGTGCATGGCGA 25

244 CGAACCAGGCGACGTGCATGGCGA 268

RESULT 6

LOCUS R53330 469 bp mRNA linear EST 18-MAY-1995

DEFINITION YG83b02.r1 Soares infant brain INIB Homo sapiens cDNA clone

IMAGE:39920 5', similar to gb:M23234 MULTIDrug RESISTANCE PROTEIN 3

(HUMAN), mRNA sequence.

R53330

EST.

R53330.1 GI:815232

EST.

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EST.

I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5].
 AACTGAGAATTCGGCCGACAGATTTTCTTTTCTTTTCTTTT 3');
 double-stranded cDNA was ligated to Hind III adaptor (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lambda B4 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 25; DB 7; Length 469;
 Best Local Similarity 100.0%; Pred. No. 0.99;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
 |||||
 Db 242 CGAACGAGGCGACGTGCATGGCGA 266

RESULT 7

BP243819/c 568 bp mRNA linear EST 15-SEP-2004
 LOCUS BP243819 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone
 DEFINITION BP243819, mRNA sequence.
 ACCESSION BP243819
 VERSION BP243819.1 GI:52116729
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 568)
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers

FEATURES

source 1..568
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEP21483"
 /issue_type="liver"
 /cell_line="HepG2"
 /clone_lib="Sugano cDNA library, liver HepG2"
 /note="hepatoma"

ORIGIN

Query Match 100.0%; Score 25; DB 5; Length 568;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
 |||||
 Db 156 CGAACGAGGCGACGTGCATGGCGA 132

RESULT 8

BP220580/c 570 bp mRNA linear EST 15-SEP-2004
 LOCUS BP220580 Sugano cDNA library, colon Homo sapiens cDNA clone
 DEFINITION BP220580, mRNA sequence.
 ACCESSION BP220580
 VERSION BP220580.1 GI:52093485
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 570)
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers

FEATURES

source 1..570
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="COL03695"
 /issue_type="colon"
 /clone_lib="Sugano cDNA library, colon"

ORIGIN

Query Match 100.0%; Score 25; DB 5; Length 570;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGAACGAGGCGACGTGCATGGCGA 25
 |||||
 Db 245 CGAACGAGGCGACGTGCATGGCGA 221

RESULT 9

AG179058/c 669 bp DNA linear GSS 09-JAN-2002
 LOCUS AG179058 Pan troglodytes DNA, clone: RP43-051D12.T7, genomic survey sequence.
 DEFINITION AG179058
 ACCESSION AG179058
 VERSION AG179058.1 GI:16708738
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE BAC end sequences of library RP43-43
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 669)
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 COMMENT (E-mail:chimps@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RP43-43 This BAC end was generated during the Rad process and may have higher chance of clone tracking errors.
 PRIMERS

Sequencing: T7
 LIBRARY Vector : pBACe3.6
 R.site 1 : EcoRI
 R.site 2 : EcoRI.
 Location/Qualifiers

FEATURES

source 1..669
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-051D12.T7"

```

/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
ORIGIN
Query Match      100.0%; Score 25; DB 9; Length 669;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 CGAACCGGCGCAGTGCATGCGCA 25
|||||
162 CGAACCGGCGCAGTGCATGCGCA 138

RESULT 10
AG179442      699 bp      DNA      linear      GSS 09-JAN-2002
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-051L12.T7, genomic survey
sequence.
ACCESSION
AG179442
VERSION
AG179442.1
KEYWORDS
GI:16709122
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H., and Sakaki, Y.
BAC end sequences of Library RPCI-43
Unpublished
2 (bases 1 to 699)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H., and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Ageo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suehiro-chou, Tsutsumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimbee@res.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EORI
R.Site 2 : EORI.
Location/Qualifiers
1..699
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-051L12.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
ORIGIN
Query Match      100.0%; Score 25; DB 9; Length 699;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 CGAACCGGCGCAGTGCATGCGCA 25
|||||
150 CGAACCGGCGCAGTGCATGCGCA 126

RESULT 11
AY408954      3843 bp      DNA      linear      GSS 15-DEC-2003
LOCUS
DEFINITION
Homo sapiens ABCB1 gene, VIRUTAL TRANSCRIPT, partial sequence,

```

```

genomic survey sequence.
AY408954      3843 bp      DNA      linear      GSS 15-DEC-2003
LOCUS
DEFINITION
Pan troglodytes ABCB1 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY408955
VERSION
AY408955.1
KEYWORDS
GI:39764922
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1..3843
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..3843
/clone="ABCB1"
/locus_tag="HCBM3396"
ORIGIN
Query Match      100.0%; Score 25; DB 9; Length 3843;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 CGAACCGGCGCAGTGCATGCGCA 25
|||||
1640 CGAACCGGCGCAGTGCATGCGCA 1616

RESULT 12
AY408955      3843 bp      DNA      linear      GSS 15-DEC-2003
LOCUS
DEFINITION
Pan troglodytes ABCB1 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY408955
VERSION
AY408955.1
KEYWORDS
GI:39764923
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
1 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission

```

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
 FEATURES Location/Qualifiers
 source 1..3843
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 <1..3843
 /gene="ABCB1"
 /locus_tag="HCM3396"
 ORIGIN
 Query Match 100.0%; Score 25; DB 9; Length 3843;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAACCAGGCGCAGTCGATGGCGA 25
 |||||
 Db 1640 CGAACCAGGCGCAGTCGATGGCGA 1616
 |||||
 RESULT 13
 BC042531/c 4035 bp mRNA linear HTC 06-JAN-2003
 LOCUS Homo sapiens, ATP-binding cassette, sub-family B (MDR/TAP), member
 DEFINITION 4. clone IMAGE:4837724, mRNA.
 ACCESSION BC042531
 VERSION BC042531.1 GI:27503509
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 4035)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (02-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA
 REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
 COMMENT Contact: MGC help desk
 Email: cgabs-rc@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
 FEATURES
 source 1..4035
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4837724"
 /tissue_type="Testis"
 /clone_id="NH_MGC_97"
 /lab_host="DH10B"
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
 Series: IRAX Plate: 72 Row: 1 Column: 3
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9961253
 This clone has the following problem: frame shifted.
 Location/Qualifiers

ORIGIN /note="Vector: pbluescript"
 Query Match 100.0%; Score 25; DB 3; Length 4035;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGAACCAGGCGCAGTCGATGGCGA 25
 |||||
 Db 1758 CGAACCAGGCGCAGTCGATGGCGA 1734
 |||||
 RESULT 14
 AG179392/c 680 bp DNA linear GSS 09-JAN-2002
 LOCUS Pan troglodytes DNA, clone: RP43-051K1.17, genomic survey
 DEFINITION sequence.
 ACCESSION AG179392
 VERSION AG179392.1 GI:16709072
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 REFERENCE 1
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE BAC end sequences of Library RPCI-43
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 680)
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suenihiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpanse@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
 PRIMERS
 Sequencing: T7
 LIBRARY
 Vector : pBAC3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI
 Location/Qualifiers
 source 1..680
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-051K1.17"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_id="RPCI-43 Chimpanzee Male BAC Library"
 ORIGIN
 Query Match 93.6%; Score 23.4; DB 9; Length 680;
 Best Local Similarity 96.0%; Pred. No. 5.6;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGAACCAGGCGCAGTCGATGGCGA 25
 |||||
 Db 125 CGAACCAGGCGCAGTCGATGGCGA 101
 |||||
 RESULT 15
 AV191114 360 bp mRNA linear EST 22-JUL-1999
 LOCUS AV191114
 DEFINITION AV191114 Yui Kohara unpublished cDNA: Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone YK590b5 5', mRNA sequence.
 ACCESSION AV191114

VERSION AV191114.1 GI:5573266
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans

REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Shii-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuiki,H.,
Nishigaki,A., Motomashi,T., Zeng,Q., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.

TITLE Expressed genes in C.elegans
JOURNAL Unpublished (1999)
COMMENT Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source location/Qualifiers
1..360
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="YK590D5"
/sex="hermaphrodite"
/dev_stages="embryo"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"

ORIGIN
Query Match 80.8%; Score 20.2; DB 1; Length 360;
Best Local Similarity 88.0%; Pred.No.1.5e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAACGAGGCGACGTGCAATGGCGA 25
|||||
DB 303 CGAACGAGGCGACGTGCAATGGAGA 327

Search completed: February 9, 2005, 21:55:45
Job time : 2451.85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 481.178 Seconds
(without alignments)
2517.530 Million cell updates/sec

Title: US-10-007-255-15
Perfect score: 25
Sequence: 1 gcttgcacacacgacacacacacac

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_rgs:*
12: gb_by:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	AX504312	AX504312 Sequence
2	25	100.0	25	AX504329	AX504329 Sequence
3	25	100.0	210	HUMMDR1A14	M29435 Human P-gly
4	25	100.0	2726	133621	I33621 Sequence 1
5	25	100.0	3840	AX481416	AX481416 Sequence
6	25	100.0	3843	BD171402	BD171402 Method fo
7	25	100.0	3860	AX322787	AX322787 Sequence
8	25	100.0	3860	AX322789	AX322789 Sequence
9	25	100.0	3988	BD190394	BD190394 Phosphat
10	25	100.0	3988	AR452556	AR452556 Sequence
11	25	100.0	3988	AX024454	AX024454 Sequence
12	25	100.0	4192	AF016535	AF016535 Homo sapi
13	25	100.0	4264	AR051647	AR051647 Sequence
14	25	100.0	4264	AR051650	AR051650 Sequence
15	25	100.0	4378	E02326	E02326 Multidrug r
16	25	100.0	4553	CO716151	CO716151 Sequence
17	25	100.0	4643	CO815440	CO815440 Sequence
18	25	100.0	4643	AX522070	AX522070 Sequence
19	25	100.0	4643	AX587788	AX587788 Sequence

c	20	25	100.0	4646	6	BD234195	BD234195 ATP-bind
c	21	25	100.0	4646	6	CO861565	CO861565 Sequence
c	22	25	100.0	4646	6	I49610	I49610 Sequence 2
c	23	25	100.0	4646	6	AR380622	AR380622 Sequence
c	24	25	100.0	4646	6	AX336420	AX336420 Sequence
c	25	25	100.0	4646	6	AX336708	AX336708 Sequence
c	26	25	100.0	4646	6	AX391099	AX391099 Sequence
c	27	25	100.0	4646	6	AX504298	AX504298 Sequence
c	28	25	100.0	4646	6	HUMMDR1	M14758 Homo sapien
c	29	25	100.0	4669	6	AX091275	AX091275 Sequence
c	30	25	100.0	4669	6	I08557	I08557 Sequence 3
c	31	25	100.0	4669	6	AR203322	AR203322 Sequence
c	32	25	100.0	4669	6	AR363344	AR363344 Sequence
c	33	25	100.0	4669	6	AR405961	AR405961 Sequence
c	34	25	100.0	6505	6	AR028671	AR028671 Sequence
c	35	25	100.0	8630	6	AR306491	AR306491 Sequence
c	36	25	100.0	8630	6	AR306492	AR306492 Sequence
c	37	25	100.0	8630	6	AX012320	AX012320 Sequence
c	38	25	100.0	8630	6	AX012321	AX012321 Sequence
c	39	25	100.0	9318	6	AR028672	AR028672 Sequence
c	40	25	100.0	98472	6	AX706975	AX706975 Sequence
c	41	25	100.0	98472	6	AC005068	AC005068 Homo sapi
c	42	25	100.0	98472	6	AX706983	AX706983 Sequence
c	43	25	100.0	128993	6	AX706983	AX706983 Sequence
c	44	25	100.0	128993	6	AX707913	AX707913 Sequence
c	45	25	100.0	147436	2	AC079303	AC079303 Homo sapi

ALIGNMENTS

RESULT 1
AX504312
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX504312
Sequence 15 from Patent WO0234291.
AX504312
AX504312.1 GI:23386130
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
location/Qualifiers
1. 25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.04; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0;

QY 1 GCTTGTGATCCACGACACTCTTAC 25
|||||
Db 1 GCTTGTGATCCACGACACTCTTAC 25

RESULT 2
AX504329/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX504329
Sequence 32 from Patent WO0234291.
AX504329
AX504329.1 GI:23386141
Homo sapiens (human)
Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS 1 Colgan, S.P.

JOURNAL Multiple drug resistance

FEATURES Patent: WO 02344291-A 32 02-MAY-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)

SOURCE location/Qualifiers

1. .25

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCAGCAGCACTCTCTAC 25

Db 25 GCTTGTGATCCAGCAGCACTCTCTAC 1

RESULT 3 HUMMDR1A14/c

LOCUS HUMMDR1A14 210 bp DNA linear PRI 08-JAN-1995

DEFINITION Human P-glycoprotein (MDR1) gene, exon 16.

ACCESSION M29435.1 GI:187484

VERSION M29435.1 GI:187484

KEYWORDS P-glycoprotein; multidrug resistance.

SEGMENT 14 of 26

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 210)

AUTHORS Chen, C.-J., Clark, D., Ueda, K., Pastan, I., Gottesman, M.M. and Robinson, I.B.

TITLE Genomic organization of the human multidrug resistance (MDR1) gene and origin of P-glycoprotein

JOURNAL J. Biol. Chem. 265 (1), 506-514 (1990)

MEDLINE 90094448

PUBMED 1967175

COMMENT Original source text: Human multidrug resistant cell line KB-VL DNA.

Draft entry and computer-readable sequence for [1] kindly submitted by I.B.Robinson, 27-OCT-1989.

Location/Qualifiers

1. .210

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="7q21"

/feature="7q21"

/gene="PGY1"

/note="PGY1 mRNA and introns"

<1. .17

/gene="PGY1"

/note="PGY1, intron O"

18. .194

/gene="PGY1"

/note="P-glycoprotein; G00-120-712"

/number=16

195. .>210

/gene="PGY1"

/note="PGY1, intron P"

ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 210;

Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCAGCAGCACTCTCTAC 25

Db 160 GCTTGTGATCCAGCAGCACTCTCTAC 136

RESULT 4 I33621

LOCUS I33621/c 2726 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 1 from patent US 5593840.

ACCESSION I33621

VERSION I33621.1 GI:1824412

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2726)

AUTHORS Bhattachar, S.K., George, A.L., Jr. and Nazarenko, I.

JOURNAL Amplification of nucleic acid sequences

FEATURES Patent: US 5593840-A 1 14-JAN-1997;

source location/Qualifiers

1. .2726

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 2726;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCAGCAGCACTCTCTAC 25

Db 534 GCTTGTGATCCAGCAGCACTCTCTAC 510

RESULT 5 AX481416

LOCUS AX481416 3840 bp DNA linear PAT 16-AUG-2002

DEFINITION Sequence 30 from Patent WO02055693.

ACCESSION AX481416

VERSION AX481416.1 GI:22316330

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1

AUTHORS Kreutzger, R., Limmer, S., Rost, S. and Hadwiger, P.

TITLE Method for inhibiting the expression of a target gene

JOURNAL Patent: WO 02055693-A 30 18-JUL-2002;

Ribopharma AG (DE)

Location/Qualifiers

1. .3840

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 3840;

Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCAGCAGCACTCTCTAC 25

Db 2027 GCTTGTGATCCAGCAGCACTCTCTAC 2003

RESULT 6 BD171402

LOCUS BD171402/c 3843 bp DNA linear PAT 18-FEB-2003

DEFINITION Method for predicting side effects of immunosuppressant and primer used therefor.

ACCESSION BD171402

VERSION BD171402.1 GI:28412692

KEYWORDS	JP 2002223769-A/1.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 3843)
TITLE	Ielrj,I.
JOURNAL	Method for predicting side effects of immunosuppressant and primer used therefor Patent: JP 2002223769-A 1 13-AUG-2002;
COMMENT	SRL INC
OS	Homo sapiens (human)
PN	JP 2002223769-A/1
PD	13-AUG-2002
PF	31-JAN-2001 JP 2001024723
PI	ICHIRO IELRI
PC	C12N15/09,C12Q1/68,C12N15/00
CC	Method for predicting side effects of immunosuppressant and primer used
CC	therefor
FH	key
FT	source
FEATURES	Location/Qualifiers FT 1..3843 /organism='Homo sapiens (human)'. /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'
ORIGIN	
Query Match	100.0%; Score 25; DB 6; Length 3843;
Best Local Similarity	100.0%; Pred. No. 0.047;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GCTTGTGATCCACGCAGCACTCCTAC 25
Db	2030 GCTTGTGATCCACGCAGCACTCCTAC 2006
RESULT 7	
LOCUS	AXJ22787/c 3860 bp DNA linear PAT 07-JAN-2002
DEFINITION	Sequence 1 from Patent WO0192877.
ACCESSION	AXJ22787
VERSION	AXJ22787.1 GI:18093766
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 Sorrentino,B. and Schuetz,J.
TITLE	Method of identifying and/or isolating stem cells
JOURNAL	Patent: WO 0192877-A 1 06-DEC-2001; ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
FEATURES	Location/Qualifiers source 1..3860 /organism='Homo sapiens' /mol_type='unassigned DNA' /db_xref='taxon:9606'
ORIGIN	
Query Match	100.0%; Score 25; DB 6; Length 3860;
Best Local Similarity	100.0%; Pred. No. 0.047;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 GCTTGATCCACGCAGCACTCCTAC 25
Db	2030 GCTTGATCCACGCAGCACTCCTAC 2006
RESULT 8	
AXJ22789/c	

LOCUS	AX322789	3860 bp	DNA	linear	PAT 07-JAN-2002
DEFINITION	Sequence 3 from Patent WO0192877.				
ACCESSION	AX322789				
VERSION	AX322789.1	GI:18093767			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 Sorrentino, B. and Schuetz, J.				
AUTHORS	Method of identifying and/or isolating stem cells				
TITLE	Patent: WO 0192877-A 3 06-DEC-2001;				
JOURNAL	ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)				
FEATURES	Location/Qualifiers				
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Best Local Similarity	100.0%;	Pred. No. 0.047;			
Matches	25;	Conservative 0;	Indels 0;	Gaps 0;	
OY	1 GCTTGTGATCCAGGACACTCTCTAC 25				
Db	2030 GCTTGTGATCCAGGACACTCTCTAC 2006				
RESULT 9					
LOCUS	BD190394	3988 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Phosphatidylcholine as a medicament for the protection of mucosa.				
ACCESSION	BD190394				
VERSION	BD190394.1	GI:33000133			
KEYWORDS	JP 2002522381-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 3988)				
AUTHORS	Stremmel, W.				
TITLE	Phosphatidylcholine as a medicament for the protection of mucosa				
JOURNAL	Patent: JP 2002522381-A 1 23-JUL-2002;				
COMMENT	Wolfgang STREMMEI.				
	OS Homo Sapiens				
	PN JP 2002522381-A/1				
	PD 23-JUL-2002				
	PF 06-AUG-1999 JP 2000563262				
	PR 06-AUG-1998 DE 198 35 526.2, 15-DEC-1998 DE 198 57 750.8 PI				
	Wolfgang stremmel				
	CC				
FEATURES	FH Key Location/Qualifiers.				
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	/db_xref="taxon:9606"				
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Query Match	100.0%;	Score 25;	DB 6;	Length 3988;	
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Matches	25;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 GCTTGTGATCCAGGACACTCTCTAC 25				
Db	2036 GCTTGTGATCCAGGACACTCTCTAC 2072				
RESULT 10					
LOCUS	AR452556	3988 bp	DNA	linear	PAT 20-FEB-2004

DEFINITION Sequence 1 from patent US 6677319.
ACCESSION AR452556
VERSION AR452556.1 GI:42684344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3988)
AUTHORS Stremmel, W.
TITLE Phosphatidylcholine as medication with protective effect large intestine mucosa
JOURNAL Patent: US 6677319-A 1 13-JAN-2004;
FEATURES location/Qualifiers
1..3988
/organism="unknown"
/mol_type="genomic DNA"

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Query Match 100.0%; Score 25; DB 6; Length 3988;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTATCCACGACACTCTTAC 25
Db 2096 GCTTGTATCCACGACACTCTTAC 2072

RESULT 11
AX024454/c 3988 bp DNA linear PAT 15-SEP-2000
LOCUS AX024454
DEFINITION Sequence 1 from Patent DE19857750.
ACCESSION AX024454
VERSION AX024454.1 GI:10184622
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Stremmel, W.
JOURNAL Patent: DE 19857750-A 1 24-FEB-2000;
FEATURES STREMMEL WOLFGANG (DE)
location/Qualifiers
1..3988
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/note="MDRI/menschliche MDR-Genfamilie"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 3988;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTATCCACGACACTCTTAC 25
Db 2096 GCTTGTATCCACGACACTCTTAC 2072

RESULT 12
AF016535/c 4192 bp mRNA linear PRI 03-SEP-1997
LOCUS AF016535
DEFINITION Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds.
ACCESSION AF016535
VERSION AF016535.1 GI:2353263
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 4192)
AUTHORS Chen, C.-Y., Chin, J.-B., Ueda, K., Clark, D. P., Pastan, I., Gottesman, M. M. and Roninson, I. B.

TITLE Internal duplication and homology with bacterial transport proteins in the mdr1 (P-glycoprotein) gene from multidrug-resistant human cells
JOURNAL Cell 47 (3), 381-389 (1986)
MEDLINE 87028230
PUBMED 2876781
REFERENCE 2 (bases 1 to 4192)
AUTHORS Chen, G., Duran, G.E., Steger, K.A., Lacayo, N.J., Jaffrezou, J.P., Dumontet, C. and Sikic, B.I.
TITLE Multidrug-resistant human sarcoma cells with a mutant P-glycoprotein, altered phenotype, and resistance to cyclosporins
JOURNAL J. Biol. Chem. 272 (9), 5974-5982 (1997)
MEDLINE 97190336
PUBMED 9038218
REFERENCE 3 (bases 1 to 4192)
AUTHORS Chen, G., Lacayo, N.J., Steger, K.A. and Sikic, B.I.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1997) Medicine, Stanford University School of Medicine, Stanford, CA 94306, USA
FEATURES location/Qualifiers
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120..3959
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/product="P-glycoprotein"
/protein_id="AA069423.1"
/db_xref="GI:2353264"

/translation="MDLEGRNGAGKRPFLNKKSEKKKKKPTTVSVFSEFRSN
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GMFEDVDVDELNTPLTDVSKINEGIDGIMGFQSMATFFGFIIVFGWMLTTLVI
LAISPLVGLSAVMAKILSSPTDKDLAVAKGAVAEVLAIRVIAFGGQKKEER
VKNLEEARIGIKKAITANISIGAEFLIVSYLAAPVGGTIVSGVSGQVLT
FVYLIGARVQGASPSIEAFANRGAATIFKIIDKPSIDTSKSGKPNIKNLE
FNVHRSYSRREVKILKGLNLKQVSGTVALVNSGCKSTTVQIMQRLYDTEGV
SVNGODIRITINVRFLREIIGVSOEPLVATTAENIRYGRBNVMDTEKVEKNA
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VVOVLDKARKKRTTIVIAHRLSTVRNAVIGFDDGVIVKGNHDELMKKEGITYKL
VMOVAGNVELENADESKRIIDALEMNSDSRSLSIKRSTRBSVRSGQADPVL
TKBALDESIPVSPFRINKLNTMPYFVYGFCAIINGLQPAPIITISKITGVTR
IDDPETKQNSNLFSLLFLALGITSITPFLGFTFGKAGLITKRLRVRFSWLRQ
DVSFDDPKNTTGALTTRLANDAAOVKAGISGLAVITVINANLGIITISLYGQI
TLALLAIYPIIALAGVEMKLSGOALKQKLEGGKATATENFRIVLSLTQOK
FEHMYAOSLOVPEYRNSLRKAHFGITFSTQAMMFESYCGRFAYIVAAHKMSPE
VILVPSAVVGEAMAVGVSFADYAKAKISAAHIIMITEKPLIDSYSTEGMPTL
EENVTGFEVENVPTRPDIPIVUGLSLEVKQQTALVSSSGCGSTVQLLERFDP
LAGKVLDDKEIKRLNVQMLRAHLGIVSQEPLTFQCSIAENIAYGNSNVVQEEIVR
LAKENINAHFIESLPNKYSTKVGDKTQSGGQKORIALAPALVRPHILLDEATSA
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1351
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variation
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673..674
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variation
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variation
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ORIGIN

Query Match 100.0%; Score 25; DB 9; Length 4192;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTCTAC 25
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Db 2146 GCTTGTGATCCACGACACTCTCTAC 2122

RESULT 13

AR051647/c 4264 bp DNA linear PAT 29-SEP-1999
LOCUS AR051647
DEFINITION Sequence 1 from patent US 5830697.
ACCESSION AR051647
VERSION AR051647.1 GI:5975011
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 4264)
AUTHORS Slikic, B.I. and Chen, G.
TITLE P-glycoprotein mutant resistant to cyclosporin modulation
JOURNAL Patent: US 5830697-A 1 03-NOV-1998;
FEATURES Location/Qualifiers
Source 1. 4264
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 4264;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTCTAC 25
|||||
Db 2168 GCTTGTGATCCACGACACTCTCTAC 2144

RESULT 14

AR051650/c 4264 bp DNA linear PAT 29-SEP-1999
LOCUS AR051650
DEFINITION Sequence 5 from patent US 5830697.
ACCESSION AR051650
VERSION AR051650.1 GI:5975014
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 4264)
AUTHORS Slikic, B.I. and Chen, G.
TITLE P-glycoprotein mutant resistant to cyclosporin modulation
JOURNAL Patent: US 5830697-A 5 03-NOV-1998;
FEATURES Location/Qualifiers
Source 1. 4264
/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 4264;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTCTAC 25
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Db 2168 GCTTGTGATCCACGACACTCTCTAC 2144

RESULT 15
E02326/c 4378 bp RNA linear PAT 29-SEP-1997
LOCUS E02326
DEFINITION Multidrug resistance relating gene derived from human normal cells.
ACCESSION E02326
VERSION E02326.1 GI:2170561
KEYWORDS JP 1990100680-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 4378)
AUTHORS Ueda, K. and Komano, T.
TITLE HUMAN NORMAL CELL-DERIVED MDR RELATED GENE
JOURNAL Patent: JP 1990100680-A 1 12-APR-1990;
SUNTORY LTD

COMMENT
OS Homo sapiens
PN JP 1990100680-A/1
PD 12-APR-1990
PF 05-OCT-1988 JP 1988251475
PI UEDA KAZUMITSU, KOMANO TORU
PC C12N15/12,C12N1/21,C12Q1/68;
CC strandedness: Single;
CC topology: Linear;
CC *source: tissue type=Adrenal gland;
CC *source: clone=SAM1132;
FH Key Location/Qualifiers

FT 5'UTR 1..137
FT CDS 138..3980
FT FT /gene='Multidrug resistance relating gene' FT
FT mat_peptide 138..3977
FT /gene='MDR1' FT

FEATURES
source Location/Qualifiers
1..4378
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 4378;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTCTAC 25
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Db 2167 GCTTGTGATCCACGACACTCTCTAC 2143

Search completed: February 9, 2005, 17:02:02
Job time : 481.178 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 : Search time 78.592 Seconds
(without alignments)
520.498 Million cell updates/sec

Title: US-10-007-255-15

Perfect score: 25
Sequence: 1 gcttcgacacagcagcaccctctac 25

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
C 1	25	100.0	2726 1	US-08-461-823-1 Sequence 1, Appli
C 2	25	100.0	3988 4	US-09-762-195-1 Sequence 1, Appli
C 3	25	100.0	4264 2	US-08-784-649A-1 Sequence 1, Appli
C 4	25	100.0	4264 2	US-08-784-649A-5 Sequence 5, Appli
C 5	25	100.0	4646 1	US-08-181-471-2 Sequence 2, Appli
C 6	25	100.0	4646 4	US-09-023-655-1167 Sequence 1167, Ap
C 7	25	100.0	4669 2	US-08-752-447-1 Sequence 1, Appli
C 8	25	100.0	4669 3	US-09-315-167-1 Sequence 1, Appli
C 9	25	100.0	4669 4	US-09-397-233-1 Sequence 1, Appli
C 10	25	100.0	4669 6	5206352-3 Patent No. 5206352
C 11	25	100.0	4669 6	5206352-3 Patent No. 5206352
C 12	25	100.0	6505 2	US-08-793-610-5 Sequence 5, Appli
C 13	25	100.0	8630 4	US-09-306-417-1 Sequence 1, Appli
C 14	25	100.0	8630 4	US-09-306-417-2 Sequence 2, Appli
C 15	25	100.0	9318 2	US-08-793-610-6 Sequence 6, Appli
C 16	24	96.0	4186 4	US-09-672-810-1 Sequence 1, Appli
C 17	24	96.0	4195 4	US-09-672-810-3 Sequence 3, Appli
C 18	23.4	93.6	4659 2	US-08-583-276-18 Sequence 18, Appli
C 19	17.6	70.4	175236 4	US-09-949-016-1453 Sequence 1453, A
C 20	17	68.0	601 4	US-09-949-016-86814 Sequence 86814, A
C 21	17	68.0	606 4	US-09-252-991A-3463 Sequence 3463, Ap
C 22	17	68.0	1713 4	US-09-252-991A-3439 Sequence 3439, Ap
C 23	17	68.0	2112 4	US-09-252-991A-3494 Sequence 3494, Ap
C 24	17	68.0	2127 4	US-09-252-991A-3450 Sequence 3450, Ap
C 25	17	68.0	24204 4	US-09-949-016-16232 Sequence 16232, A
C 26	17	68.0	247781 4	US-09-949-016-14193 Sequence 14193, A
C 27	16.6	66.4	601 4	US-09-949-016-205911 Sequence 205911, A

28	16.6	66.4	601	4	US-09-949-016-205912	Sequence 205912, A
29	16.6	66.4	57761	4	US-09-949-016-13429	Sequence 13429, A
C 30	16.6	66.4	74644	4	US-09-949-016-17556	Sequence 17556, A
31	16.2	64.8	246	4	US-09-252-991A-11850	Sequence 11850, A
32	16.2	64.8	601	4	US-09-949-016-174875	Sequence 174875, A
33	16.2	64.8	601	4	US-09-949-016-174876	Sequence 174876, A
34	16.2	64.8	792	4	US-09-252-991A-11705	Sequence 11705, A
35	16.2	64.8	876	4	US-09-252-991A-11783	Sequence 11783, A
C 36	16.2	64.8	975	4	US-09-252-991A-11651	Sequence 11651, A
C 37	16.2	64.8	1083	4	US-09-252-991A-11533	Sequence 11533, A
38	16.2	64.8	16373	4	US-09-949-016-12820	Sequence 12820, A
C 39	16.2	64.8	16373	4	US-09-949-016-16897	Sequence 16897, A
C 40	16.2	64.8	45840	4	US-09-949-016-13903	Sequence 13903, A
C 41	16.2	64.8	45840	4	US-09-949-016-15042	Sequence 15042, A
C 42	16.2	64.8	46559	4	US-09-949-016-15043	Sequence 15043, A
C 43	16.2	64.8	49971	4	US-09-949-016-16688	Sequence 16688, A
44	16	64.0	19	4	US-08-820-479-6	Sequence 6, Appli
45	16	64.0	601	4	US-09-949-016-26189	Sequence 26189, A

ALIGNMENTS

RESULT 1
US-08-461-823-1/c
Sequence 1, Application US/08461823
Patent No. 5593840
GENERAL INFORMATION:
APPLICANT: Bhatnagar, Satish K.
APPLICANT: George Jr., Albert L.
APPLICANT: Nazarenko, Irina
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: OncorPharm, Inc.
STREET: 200 Perry Parkway
CITY: Gaithersburg
STATE: Maryland
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,823
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/168,621
FILING DATE: 16-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,433
FILING DATE: 27-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kaita, Glenn E.
REGISTRATION NUMBER: 30,649
REFERENCE/DOCKET NUMBER: PA-0012 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301 527-2058
TELEFAX: 301 208-6997
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-461-823-1

Query Match 100.0%; Score 25; DB 1; Length 2726;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGGACACTCTTAC 25
DB 534 GCTTGTGATCCAGGACACTCTTAC 510

RESULT 2

US-09-762-195-1/c
Sequence 1, Application US/09762195
Patent No. 6677319
GENERAL INFORMATION:
APPLICANT: Stemmel, Wolfgang
TITLE OF INVENTION: Phosphatidylcholine as Medication with
FILE REFERENCE: 34691/208520
CURRENT FILING DATE: US/09/762,195
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/EP9702426
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 198 57 570.8 DE
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ. ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3988
TYPE: DNA
ORGANISM: Homo sapiens
US-09-762-195-1

Query Match 100.0%; Score 25; DB 4; Length 3988;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGGACACTCTTAC 25
DB 2096 GCTTGTGATCCAGGACACTCTTAC 2072

RESULT 3

US-08-784-649A-1/c
Sequence 1, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: Sikic, Branimir I
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-784-649A-1

Query Match 100.0%; Score 25; DB 2; Length 4264;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGGACACTCTTAC 25
DB 2168 GCTTGTGATCCAGGACACTCTTAC 2144

RESULT 4

US-08-784-649A-5/c
Sequence 5, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: Sikic, Branimir I
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-784-649A-5

Query Match 100.0%; Score 25; DB 2; Length 4264;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGGACACTCTTAC 25
DB 2168 GCTTGTGATCCAGGACACTCTTAC 2144

RESULT 5

US-08-181-471-2/c
 ; Sequence 2, Application US/08181471
 ; Patent No. 5641508
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Lingna
 ; TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
 ; TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Thomas Fitting
 ; STREET: 12526 High Bluff Drive, Suite 300
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92130
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/181,471
 ; FILING DATE: 13-JAN-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/041,553
 ; FILING DATE: 02-APR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fitting, Thomas
 ; REGISTRATION NUMBER: 34,163
 ; REFERENCE/DOCKET NUMBER: ANT0029P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-792-3680
 ; TELEFAX: 619-792-8477
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4646 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 425..4267
 ; US-08-181-471-2

Query Match 100.0%; Score 25; DB 1; Length 4646;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGCAGACTCTCTAC 25
 ||||||||||||||||||||||||||||
 DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 6
 US-09-023-655-1167/c
 ; Sequence 1167, Application US/09023655.
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO

STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1167:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4646 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g187468
 US-09-023-655-1167

Query Match 100.0%; Score 25; DB 4; Length 4646;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGCAGACTCTCTAC 25
 ||||||||||||||||||||||||||||
 DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 7
 US-08-752-447-1/c
 ; Sequence 1, Application US/08752447
 ; Patent No. 5994088
 ; GENERAL INFORMATION:
 ; APPLICANT: Mechtner, Eugene
 ; APPLICANT: Robinson, Igor B
 ; TITLE OF INVENTION: Methods and Reagents for Preparing and
 ; TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boehrnen Hulbert & Berghoff Ltd.
 ; STREET: 300 South Wacker Drive, Seventh Floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/752,447
 ; FILING DATE: 15-NOV-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5994088nam, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 95,1121

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-08-752-447-1

Query Match 100.0%; Score 25; DB 2; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGATCCAGCAGACTCTCTAC 25
Db 2454 GCTTGATCCAGCAGACTCTCTAC 2430

RESULT 8

US-09-316-167-1/c
Sequence 1, Application US/09316167
Patent No. 6365357
GENERAL INFORMATION:
APPLICANT: Mechtner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316.167
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752.447
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. 6365357nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
US-09-316-167-1

Query Match 100.0%; Score 25; DB 3; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGATCCAGCAGACTCTCTAC 25
Db 2454 GCTTGATCCAGCAGACTCTCTAC 2430

RESULT 9

US-09-397-233-1/c
Sequence 1, Application US/09397233
Patent No. 6630327
GENERAL INFORMATION:
APPLICANT: Mechtner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397.233
FILING DATE: 16-Sep-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6630327nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-397-233-1

Query Match 100.0%; Score 25; DB 4; Length 4669;

Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGATCCAGCAGACTCTCTAC 25
DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 10
5206352-3/c
Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman, Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO:3:
LENGTH: 4669

Query Match 100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGATCCAGCAGACTCTCTAC 25
DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 11
5206352-3/c
Patent No. 5206352
APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman, Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
SEQ ID NO:3:
LENGTH: 4669

Query Match 100.0%; Score 25; DB 6; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGATCCAGCAGACTCTCTAC 25
DB 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 12
US-08-793-610-5/c
Sequence 5, Application US/08793610
Patent No. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARBERS, Carol

APPLICANT: OSTERTAG, Wolfram
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W., Suite 330
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6505 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA

US-08-793-610-5
Query Match 100.0%; Score 25; DB 2; Length 6505;
Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGTGATCCAGCAGACTCTCTAC 25
DB 3846 GCTTGTGATCCAGCAGACTCTCTAC 3822

RESULT 13
US-09-306-417-1/c
Sequence 1, Application US/09306417
Patent No. 6548301
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 1
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral

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/ OTHER INFORMATION: plasmid DNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(160)
/ OTHER INFORMATION: plasmid backbone (pUC)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (161)..(677)
/ OTHER INFORMATION: 5'-LTR
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: (532)..(1219)
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: (1220)..(5062)
/ OTHER INFORMATION: m4 mdr-1 cDNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5215)..(5774)
/ OTHER INFORMATION: 3'-LTR
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5775)..(8630)
/ OTHER INFORMATION: plasmid backbone (pUC)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(8630)
/ OTHER INFORMATION: retroviral expression vector SPbeta71m4
US-09-306-417-1
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Query Match          100.0%; Score 25; DB 4; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GCTTGATCCAGCAGACTCTTAC 25
Db 3249 GCTTGATCCAGCAGACTCTTAC 3225
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RESULT 14
US-09-306-417-2/c
/ Sequence 2, Application US/09306417
/ Patent No. 6548301
/ GENERAL INFORMATION:
/ APPLICANT: Heinrich-Pette-Institut
/ TITLE OF INVENTION: Retroviral Gene Transfer Vectors
/ FILE REFERENCE: P50491
/ CURRENT APPLICATION NUMBER: US/09/306,417
/ CURRENT FILING DATE: 1999-05-06
/ EARLIER APPLICATION NUMBER: DE 198 22 115
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 8630
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: proviral
/ OTHER INFORMATION: plasmid DNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(8630)
/ OTHER INFORMATION: retroviral expression vector SPbeta91MSAI
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(160)
/ OTHER INFORMATION: plasmid backbone (pUC)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (161)..(677)
/ OTHER INFORMATION: 5'-LTR
/ FEATURE:
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/ NAME/KEY: 5'UTR
/ LOCATION: (532)..(1219)
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: (1220)..(5062)
/ OTHER INFORMATION: mSAI mdr1 cDNA
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5215)..(5774)
/ OTHER INFORMATION: 3'-LTR
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (5775)..(8630)
/ OTHER INFORMATION: plasmid backbone (pUC)
US-09-306-417-2
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Query Match          100.0%; Score 25; DB 4; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3249 GCTTGATCCAGCAGACTCTTAC 3225
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RESULT 15
US-08-793-610-6/c
/ Sequence 6, Application US/08793610
/ Patent No. 5858744
/ GENERAL INFORMATION:
/ APPLICANT: BAUM, Christopher
/ APPLICANT: STOCKING-HARRIS, Carol
/ APPLICANT: OSTERFAG, Wolfram
/ TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSER: Nikaide, Marmelstein, Murray & Oram LLP
/ STREET: 655 Fifteenth Street N.W. Suite 330
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-5701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/793,610
/ FILING DATE: 07-MAR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE P 44 31 973.8
/ FILING DATE: 08-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE 195 03 952.1
/ FILING DATE: 07-FEB-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/03175
/ FILING DATE: 10-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Berman, Richard J.
/ REGISTRATION NUMBER: 39,105
/ REFERENCE/DOCKET NUMBER: P1614-7007
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)638-5000
/ TELEFAX: (202)638-4810
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9318 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: circular
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; MOLECULE TYPE: DNA
US-08-793-610-6

Query Match 100.0%; Score 25; DB 2; Length 9318;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCGACGACACTCTCTAC 25
|||||
Db 3805 GCTTGTGATCGACGACACTCTCTAC 3781

Search completed: February 9, 2005, 17:11:20
Job time : 79.592 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 266.667 Seconds
(Without alignments)
539.601 Million cell updates/sec

Title: US-10-007-255-15

Perfect score: 1
Sequence: 1 gcttgcacccacgcacactcctac 25

Scoring table: IDENTITY NUC
Gap 10.0, Gapex 1.0

Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	3840	US-10-384-339C-30	Sequence 30, Appli
2	25	100.0	3860	US-09-866-866A-1	Sequence 1, Appli
3	25	100.0	3860	US-09-866-866A-3	Sequence 3, Appli
4	25	100.0	4533	US-09-805-020-30	Sequence 30, Appli
5	25	100.0	4643	US-10-072-621-2	Sequence 2, Appli
6	25	100.0	4643	US-10-072-340-1	Sequence 1, Appli
7	25	100.0	4643	US-10-007-926A-258	Sequence 258, App
8	25	100.0	4646	US-09-968-007A-459	Sequence 459, App
9	25	100.0	4646	US-09-968-007A-747	Sequence 747, App
10	25	100.0	4646	US-10-641-643-1167	Sequence 1167, App
11	25	100.0	4646	US-10-343-657-1	Sequence 1, Appli

ALIGNMENTS

12	25	100.0	4646	US-10-775-169-198	Sequence 198, App
13	25	100.0	4669	US-10-680-516-1	Sequence 1, Appli
14	25	100.0	8630	US-09-306-417-1	Sequence 1, Appli
15	25	100.0	8630	US-09-306-417-2	Sequence 2, Appli
16	24	96.0	3852	US-10-101-431A-1	Sequence 1, Appli
17	24	96.0	4186	US-10-619-359A-1	Sequence 1, Appli
18	24	96.0	4195	US-10-619-359A-3	Sequence 3, Appli
19	19.6	78.4	31	US-09-801-274-269	Sequence 269, App
20	17.6	70.4	34	US-10-425-115-130740	Sequence 130740, App
21	17.2	68.8	625	US-10-027-632-290365	Sequence 290365, App
22	17.2	68.8	625	US-10-027-632-290365	Sequence 290365, App
23	17.2	68.8	665	US-10-027-632-126989	Sequence 126989, App
24	17.2	68.8	665	US-10-027-632-126989	Sequence 126989, App
25	17.2	68.8	1005	US-10-369-493-26051	Sequence 26051, A
26	17.2	68.8	2390	US-10-027-632-101776	Sequence 101776, App
27	17.2	68.8	2390	US-10-027-632-101776	Sequence 101776, App
28	17.2	68.8	26555	US-09-860-670-161	Sequence 161, App
29	17.2	68.8	26555	US-10-227-646-161	Sequence 161, App
30	17.2	68.8	136328	US-10-101-510-127	Sequence 127, App
31	17	68.0	388	US-10-425-115-38049	Sequence 38049, A
32	17	68.0	463	US-10-027-632-70301	Sequence 70301, A
33	17	68.0	463	US-10-027-632-70301	Sequence 70301, A
34	17	68.0	550	US-10-027-632-36762	Sequence 36762, A
35	17	68.0	550	US-10-027-632-36762	Sequence 36762, A
36	17	68.0	762	US-09-938-842A-1088	Sequence 1088, App
37	17	68.0	942	US-10-382-842A-1088	Sequence 1088, App
38	17	68.0	1198	US-10-282-122A-28884	Sequence 28884, A
39	17	68.0	1198	US-10-369-493-29334	Sequence 29334, A
40	17	68.0	1464	US-10-424-599-28742	Sequence 28742, A
41	17	68.0	1535	US-10-027-632-265708	Sequence 265708, App
42	17	68.0	1535	US-10-027-632-265708	Sequence 265708, App
43	17	68.0	1776	US-10-425-114-13600	Sequence 13600, A
44	17	68.0	1781	US-10-425-114-26722	Sequence 26722, A
45	17	68.0	1929	US-10-282-122A-29808	Sequence 29808, A

RESULT 1
US-10-384-339C-30/c

Sequence 30, Application US/10384339C
Publication No. US20040175703A1

GENERAL INFORMATION:

APPLICANT: Kreutzler, Roland

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GENE

FILE REFERENCE: 20200/2002

CURRENT FILING DATE: 2003-03-07

PRIOR FILING DATE: 2002-01-09

PRIOR APPLICATION NUMBER: DE 10100586.5

PRIOR FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: DE 10155280.7

PRIOR FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: DE 10158411.3

PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: DE 10160151.4

NUMBER OF SEQ ID NOS: 173

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30

LENGTH: 3840

TYPE: DNA

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

TITLE: mdr-1

PATENT DOCUMENT NUMBER: AF016535

US-10-384-339C-30

Query Match 100.0%; Score 25; DB 18; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGGACACTCCTAC 25
DB 2027 GCTTGTGATCCAGGACACTCCTAC 2003

RESULT 2
US-09-866-866A-1/c
; Sequence 1, Application US/09866866A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-866A-1

Query Match 100.0%; Score 25; DB 9; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTTGTGATCCAGGACACTCCTAC 25
DB 2030 GCTTGTGATCCAGGACACTCCTAC 2006

RESULT 3
US-09-866-866A-3/c
; Sequence 3, Application US/09866866A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Schuetz, John
; TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
; FILE REFERENCE: 1340-1-021CIP2
; CURRENT APPLICATION NUMBER: US/09/866,866A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/584,586
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/US99/11825
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/086,988
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-866-866A-3

Query Match 100.0%; Score 25; DB 9; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTTGTGATCCAGGACACTCCTAC 25
DB 2030 GCTTGTGATCCAGGACACTCCTAC 2006

RESULT 4
US-09-805-020-30/c
; Sequence 30, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 4533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(4533)
; OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-30

Query Match 100.0%; Score 25; DB 9; Length 4533;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTTGTGATCCAGGACACTCCTAC 25
DB 2454 GCTTGTGATCCAGGACACTCCTAC 2430

RESULT 5
US-10-072-621-2/c
; Sequence 2, Application US/10072621
; Publication No. US20020169137A1
; GENERAL INFORMATION:
; APPLICANT: Reiner, Peter B.
; APPLICANT: Connop, Bruce P.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
; FILE REFERENCE: 100103.402
; CURRENT APPLICATION NUMBER: US/10/072,621
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-621-2

Query Match 100.0%; Score 25; DB 13; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTTGTGATCCAGGACACTCCTAC 25
DB 2451 GCTTGTGATCCAGGACACTCCTAC 2427

RESULT 6
US-10-097-340-1/c
; Sequence 1, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS

APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumel ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: NRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
US-10-097-340-1

Query Match 100.0%; Score 25; DB 14; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25
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Db 2451 GCTTGTGATCCAGCAGACTCTCTAC 2427

RESULT 7
US-10-007-926A-258/c
Sequence 258, Application US/10007926A
Publication No. US20030143539A1
GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOUTIGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FERRI, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 258
LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: acp-binding cassette, sub-family b
OTHER INFORMATION: (mdr/cap), member 1 (ABCB1) gene.

US-10-007-926A-258

Query Match 100.0%; Score 25; DB 15; Length 4643;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25
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Db 2451 GCTTGTGATCCAGCAGACTCTCTAC 2427

RESULT 8
US-09-968-007A-459/c
Sequence 459, Application US/09968007A
Publication No. US20040115625A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/09/968,007A
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: PatentIn version 3.0
SEQ ID NO 459
LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
US-09-968-007A-459

Query Match 100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCAGCAGACTCTCTAC 25
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Db 2454 GCTTGTGATCCAGCAGACTCTCTAC 2430

RESULT 9
US-09-968-007A-747/c
Sequence 747, Application US/09968007A
Publication No. US20040115625A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/09/968,007A
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: PatentIn version 3.0
SEQ ID NO 747
LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
US-09-968-007A-747

PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: PatentIn version 3.0
SEQ ID NO 747
LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
US-09-968-007A-747

Query Match 100.0%; Score 25; DB 11; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGCAGCACTCTTAC 25
DB 2454 GCTTGTGATCCAGCAGCACTCTTAC 2430

RESULT 10

US-10-641-643-1167/c
Sequence 1167, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1167:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g187468
SEQUENCE DESCRIPTION: SEQ ID NO: 1167 :
US-10-641-643-1167

Query Match 100.0%; Score 25; DB 17; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTGTGATCCAGCAGCACTCTTAC 25
DB 2454 GCTTGTGATCCAGCAGCACTCTTAC 2430

DB 2454 GCTTGTGATCCAGCAGCACTCTTAC 2430

RESULT 11

US-10-343-657-1/c
Sequence 1, Application US/10343657
Publication No. US20040086882A1
GENERAL INFORMATION:
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that improve its
ability to confer resistance to chemotherapeutic drugs
FILE REFERENCE: 00,616-A
CURRENT APPLICATION NUMBER: US/10/343,657
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/222,313
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (425)...(4264)
US-10-343-657-1

Query Match 100.0%; Score 25; DB 17; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGCAGCACTCTTAC 25
DB 2454 GCTTGTGATCCAGCAGCACTCTTAC 2430

RESULT 12

US-10-775-169-198/c
Sequence 198, Application US/10775169
Publication No. US20040175743A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Dornier, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031896-013600)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 198
LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
US-10-775-169-198

Query Match 100.0%; Score 25; DB 18; Length 4646;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCAGCAGCACTCTTAC 25
DB 2454 GCTTGTGATCCAGCAGCACTCTTAC 2430

RESULT 13

US-10-680-516-1/c
Sequence 1, Application US/10680516
Publication No. US20040166110A1
GENERAL INFORMATION:

```
APPLICANT: Mechtner, Eugene
TITLE OF INVENTION: Methods and Reagents for Preparing and
Using Immunological Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/680,516
FILING DATE: 07-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,447
FILING DATE: 15-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..424
NAME/KEY: CDS
LOCATION: 425..4264
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-680-516-1

Query Match 100.0%; Score 25; DB 18; Length 4669;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCACGACACTCTCTAC 25
Db 2454 GCTTGTGATCCACGACACTCTCTAC 2430

RESULT 14
US-09-306-417-1/c
Sequence 1, Application US/09306417
Patent No. US20020103144A1
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
```

```
SEQ ID NO 1
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(160)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc feature
LOCATION: (161)..(677)
OTHER INFORMATION: 5'-LTR
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (532)..(1219)
FEATURE:
NAME/KEY: mat peptide
LOCATION: (1220)..(5062)
OTHER INFORMATION: m4 mdr-1 cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (5215)..(5774)
OTHER INFORMATION: 3'-LTR
FEATURE:
NAME/KEY: misc feature
LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SPbeta71m4
US-09-306-417-1

Query Match 100.0%; Score 25; DB 9; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTGTGATCCACGACACTCTCTAC 25
Db 3249 GCTTGTGATCCACGACACTCTCTAC 3225

RESULT 15
US-09-306-417-2/c
Sequence 2, Application US/09306417
Patent No. US20020103144A1
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 8630
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: proviral
OTHER INFORMATION: plasmid DNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SPbeta1mSA1
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(160)
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; OTHER INFORMATION: plasmid backbone (puc)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (161)..(677)
; OTHER INFORMATION: 5'-LTR
; FEATURE:
; NAME/KEY: 5' UTR
; LOCATION: (532)..(1219)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1220)..(5062)
; OTHER INFORMATION: msA1 mdr1 cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5215)..(5774)
; OTHER INFORMATION: 3'-LTR
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5775)..(8630)
; OTHER INFORMATION: plasmid backbone (puc)
US-09-306-417-2
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Query Match          100.0%; Score 25; DB 9; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTGATCCAGGAGACTCTCTAC 25
          |||||
Db      3249 GCTTGATCCAGGAGACTCTCTAC 3225
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Search completed: February 9, 2005, 22:26:43
Job time : 267.667 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:01 ; Search time 245.69 Seconds
(Without alignments)
602.360 Million cell updates/sec

Title: US-10-007-255-15
Perfect score: 25
Sequence: 1 gctctgcatccacgacacacctctac 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	AAD39004	Aad39004 Human mdr
2	25	100.0	25	AAD39014	Aad39014 Human mdr
3	25	100.0	594	ADK6076	Adk6076 Standard
4	25	100.0	2726	AAQ70907	Aaq70907 Multidrug
5	25	100.0	2726	AAQ70916	Aaq70916 Multidrug
6	25	100.0	2726	AAQ73322	Aaq73322 Multidrug
7	25	100.0	3840	ABV78146	Abv78146 Human mdr
8	25	100.0	3840	ABZ35722	Abz35722 Human mdr
9	25	100.0	3840	ABX09965	Abx09965 Human mdr
10	25	100.0	3840	ABL91687	AbL91687 Human PDI
11	25	100.0	3843	ABQ78185	AbQ78185 Human MDR
12	25	100.0	3860	AAZ49332	Aaz49332 Human w11
13	25	100.0	3860	AAZ49333	Aaz49333 Human G18
14	25	100.0	3860	ABA94365	AbA94365 Human BCR
15	25	100.0	3860	ABA94366	AbA94366 Human BCR
16	25	100.0	3988	AAZ88973	Aaz88973 Human MDR
17	25	100.0	4264	AAV65533	Aav65533 Mutated h
18	25	100.0	4264	AAV65534	Aav65534 Mutated h
19	25	100.0	4349	AAH57442	Aah57442 Human int
20	25	100.0	4378	AAQ04522	Aaq04522 Multidrug

C 21	25	100.0	4533	6	ABS65229	AbB65229 cDNA enco
C 22	25	100.0	4643	6	ABS76368	AbB76368 cDNA enco
C 23	25	100.0	4643	6	ABV94267	AbV94267 Breast ca
C 24	25	100.0	4643	6	ABV74349	AbV74349 Human ABC
C 25	25	100.0	4643	10	ABX77217	AbX77217 cDNA enco
C 26	25	100.0	4643	12	ADP18689	AdP18689 Human MDR
C 27	25	100.0	4643	12	ADO19748	AdO19748 Human PRO
C 28	25	100.0	4643	13	ADP54881	AdP54881 Human PRO
C 29	25	100.0	4646	2	AAQ72872	Aaq72872 Human mul
C 30	25	100.0	4646	3	AAZ94738	Aaz94738 Human ATP
C 31	25	100.0	4646	6	ABL68592	AbL68592 Kidney ca
C 32	25	100.0	4646	6	ABL68880	AbL68880 Kidney ca
C 33	25	100.0	4646	6	AAD38994	AdA38994 Human mdr
C 34	25	100.0	4646	10	ADK60994	AdK60994 Ovarian c
C 35	25	100.0	4646	11	ADI31841	AdI31841 Human CDN
C 36	25	100.0	4646	13	ADR52847	AdR52847 Drug ther
C 37	25	100.0	4669	1	AAAT7052	AaT7052 Sequence
C 38	25	100.0	4669	2	AAQ52726	Aaq52726 Sequence
C 39	25	100.0	4669	2	AAV32645	Aav32645 Human P g
C 40	25	100.0	4669	6	ABK52041	AbK52041 cDNA enco
C 41	25	100.0	5544	13	ACNA3504	AcN3504 Human dia
C 42	25	100.0	6505	2	AAAT3394	AaT3394 Hybrid ve
C 43	25	100.0	8630	3	AAZ24042	Aaz24042 Retrovira
C 44	25	100.0	8630	3	AAZ24041	Aaz24041 Retrovira
C 45	25	100.0	53099	6	ABS98185	AbS98185 Human mul

ALIGNMENTS

RESULT 1	AAD39004	standard; DNA; 25 BP.
ID	AAD39004	standard; DNA; 25 BP.
XX	23-SEP-2002	(first entry)
XX	Human mdr1-HRE antisense oligonucleotide #7.	
XX	Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;	
XX	hypoxia inducible factor-1; small ubiquitin-like modifier; HIF-1;	
XX	lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;	
XX	myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;	
XX	angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;	
XX	polycythaemia vera; hypoxia responsive element; HRE; antisense;	
XX	phosphorothioate backbone; ss.	
OS	Homo sapiens.	
XX	Synthetic.	
XX	Key	Location/Qualifiers
XX	modified_base	1..25
XX	FT	/*tag= a
XX	FT	/mod_base= OTHER
XX	FT	/note= "Phosphorothioate backbone"
XX	W0200234291-A2.	
XX	02-MAY-2002.	
XX	25-OCT-2001; 2001WO-US049856.	
XX	26-OCT-2000; 2000US-0243542P.	
XX	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.	
XX	Colgan SP;	
XX	WPI; 2002-471427/50.	
XX	Treating a subject (at risk of) having a hematologic malignancy or	
XX	multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia	

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
PT binding molecules.
PS Claim 14; Page 43; 92pp; English.
XX
XX The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukaemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid
CC disorders include chronic or acute myeloid leukaemia, e.g. angioleukemia
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is an antisense
CC oligo targeted to HRE in the mdrl gene (mdrl-HRE) to inhibit its
CC expression. This oligo is used in the exemplification of the invention
XX
SQ Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.06; Mismatches 0; Gaps 0;
Matches 25; Conservative 0; Indels 0; Gaps 0;
QY 1 GCTTGTGATCCACGACACTCTTAC 25
Db 1 GCTTGTGATCCACGACACTCTTAC 25
RESULT 2
AAD39014/c
ID AAD39014 standard; DNA; 25 BP.
XX
XX AAD39014;
AC
XX 23-SEP-2002 (first entry)
DT
XX
XX Human mdrl gene HIF-1 binding site DNA #7.
DE
XX
XX Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1;
KM hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1;
KM lymphoid disorder; chronic lymphoproliferative disorder; lymphoma;
KM myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma;
KM angioleukemia myeloid metaplasia; myeloid leukaemia; gene therapy;
KM polycythaemia vera; hypoxia responsive element; HRE; ds.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT misc_binding 11..15
FT /*cag= a
FT /bound_molety= "HIF-1"
XX
XX WO200234291-A2.
PN
XX
XX 02-MAY-2002.
PD
XX 25-OCT-2001; 2001WO-US049856.
PF
XX 26-OCT-2000; 2000US-0243542P.
PR
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA
XX Colgan SP;
PI
XX WPI; 2002-471427/50.
DR
XX
XX Treating a subject (at risk of) having a hematologic malignancy or
PT multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia.

PT inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
PT binding molecules.
PS Example 2; Page 12; 92pp; English.
XX
XX The invention relates to a method of treating a subject having or at risk
CC of developing a haematologic malignancy or multidrug resistance (MDR).
CC The method involves administering hypoxia inducible factor-1 (HIF-1)
CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding
CC molecules or HIF-1-SUMO-1 complex modulators. mdrl-hypoxia responsive
CC element (HRE) binding molecules or antisense nucleic acid molecules and
CC SUMO-1 binding molecules or antisense molecules are useful for treating a
CC subject having or at risk of developing haematologic malignancy or MDR
CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders
CC include lymphocytic leukemia or chronic lymphoproliferative disorders
CC e.g. lymphoma, myeloma or chronic lymphoid leukemia. The myeloid
CC disorders include chronic or acute myeloid leukemia, e.g. angioleukemia
CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The
CC invention is used in gene therapy. The present sequence is human mdrl
CC gene HIF-1 binding site DNA
XX
SQ Sequence 25 BP; 6 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.06; Mismatches 0; Gaps 0;
Matches 25; Conservative 0; Indels 0; Gaps 0;
QY 1 GCTTGTGATCCACGACACTCTTAC 25
Db 25 GCTTGTGATCCACGACACTCTTAC 1
RESULT 3
ADK66076/c
ID ADK66076 standard; RNA; 594 BP.
XX
XX ADK66076;
AC
XX 06-MAY-2004 (first entry)
DT
XX
XX Standardized polynucleotide system polynucleotide #18.
DE
XX
XX ss; standardized polynucleotide system; medical diagnosis;
KM functional genomics; sample analysis; pharmacogenomics; sample analysis.
KM
XX
XX Unidentified.
OS
XX DE10209071-A1.
PN
XX 25-SEP-2003.
PD
XX
XX 28-FEB-2002; 2002DE-01009071.
PF
XX 28-FEB-2002; 2002DE-01009071.
PR
XX (ROBO-) ROBOSCREEN GES MOLEKULARE BIOTECHNOLOGIE.
PA
XX Koehler T, Roest A;
PI
XX
XX WPI; 2003-732912/70.
DR
XX
XX Standardized polynucleotide system, useful for quantitative, real-time
PT determination of nucleic acid, comprises stabilized standards, primers
PT and probe.
XX
XX Claim 1; Page 12; 38pp; German.
PS
XX
XX The present invention relates to a standardized polynucleotide system,
CC which comprises at least one carrier nucleic acid, at least 3
CC oligonucleotides, as primers and target-specific, fluorescently labeled
CC probe and optionally at least one set of stabilized controls (standard
CC RNA or DNA) of known concentration and instructions. The system comprises
CC any of 20 sets of one control, two primers and one target-specific probe.

CC The standardized polynucleotide system can be used for quantitative, real
CC -time detection of target nucleic acids, especially analysis of genes or
CC gene products, e.g. for individualized medical diagnosis, in veterinary
CC medicine, functional genomics, clinical pharmacology, pharmacogenetics,
CC pharmaceutical testing, analysis of food or environmental samples and
CC also for ultra-sensitive detection of proteins by immuno-PCR. The present
CC sequence is a polynucleotide used in the system of the invention.

XX Sequence 594 BP; 170 A; 125 C; 131 G; 0 T; 168 U; 0 Other;

Query Match 100.0%; Score 25; DB 10; Length 594;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTCTAC 25
Db 273 GCTTGTGATCCACGACACTCTCTAC 249

RESULT 4
AAQ70907/c
ID AAQ70907 standard; DNA; 2726 BP.

XX AAQ70907;
XX 25-MAR-2003 (revised)
DT 27-MAR-1995 (first entry)

XX Multidrug-resistance gene MDR-1.

KW Multidrug-resistance; MDR-1 gene; ds.

XX Synthetic.

XX W09417206-A1.

XX 04-AUG-1994.

XX 12-NOV-1993; 93WO-US010883.

XX 27-JAN-1993; 93US-00010433.

XX (ONCO-) ONCOR INC.

PI Bhattachar SK, George AL;

XX WPI; 1994-264118/32.

XX Enzymatic amplification of target nucleic acid sequences in a mixt. - to
PT detect a mutation or allele in the target, e.g. that causes a genetic
PT disease.

PS Disclosure; Page 30; 50pp; English.

XX This gene is used as an example of a target DNA in a method for the
CC amplification of nucleic acid sequences in a mixture using various DNA
CC probes/primers. The method may be used to detect a mutation or allele in
CC the target, e.g. that causes a genetic disease. (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 2726;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTCTAC 25
Db 534 GCTTGTGATCCACGACACTCTCTAC 510

RESULT 5
AAQ70916/c

ID AAQ70916 standard; DNA; 2726 BP.

XX AAQ70916;

XX 25-MAR-2003 (revised)

DT 27-MAR-1995 (first entry)

XX Multidrug-resistance gene MDR-1.

KW Multidrug-resistance; MDR-1 gene; ds.

XX Synthetic.

XX W09417210-A1.

XX 04-AUG-1994.

XX 25-JAN-1994; 94WO-US000748.

XX 27-JAN-1993; 93US-00010433.

XX 16-DEC-1993; 93US-00168621.

XX (ONCO-) ONCOR INC.

PI Bhattachar SK, George AL;

XX WPI; 1994-264122/32.

XX Enzymatic amplification of target nucleic acid sequences to form exact or
PT modified copies - has increased fidelity and can identify point mutations
PT or allele(s).

PS Disclosure; Page 30; 69pp; English.

XX This gene is used as an example of a target DNA in a method for the
CC amplification of nucleic acid sequences in a mixture using various DNA
CC probes/primers. The method may be used to detect a mutation or allele in
CC the target, e.g. that causes a genetic disease. (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 2; Length 2726;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTTGTGATCCACGACACTCTCTAC 25
Db 534 GCTTGTGATCCACGACACTCTCTAC 510

RESULT 6

AAQ70916/c
ID AAQ70916 standard; DNA; 2726 BP.

XX AAQ70916;

XX 01-SEP-1997 (first entry)

XX Multidrug resistance gene-1.

KW PCR; primer; amplify; polymerase chain reaction; ligase chain reaction;

KW LCR; human; multidrug resistance gene; MDR-1; ds.

XX Synthetic.

XX W09639537-A1.

XX 12-DEC-1996.

XX 04-JUN-1996; 96WO-US008841.

XX 05-JUN-1995; 95US-00461823.

XX (ONCO-) ONCOR INC.
PA Bhatnagar SK, George AL, Nazarenko I;
PI WPI; 1997-043158/04.
XX
XX Amplification method avoiding strand displacement by polymerase - used in
PT the detection of mutation(s) and allele(s) associated with genetic
PT disease and cancer.
XX
XX Example 1; Page 50-51; 92pp; English.
XX
XX This sequence represents the multidrug resistance gene (MDR-1) amplified
CC by the primers shown in AAT43320 and AAT43321. This sequence can be used
CC as a target in the method of the invention, for enzymatically amplifying
CC a target nucleic acid (TNA) sequence contained in a nucleic acid or
CC mixture of nucleic acids while avoiding strand displacement by
CC polymerase. The method comprises using three primers, one complementary
CC to a first segment of the TNA, a second complementary to a second segment
CC of the TNA, which is adjacent to the first primer, and a third which is
CC similar to the first segment of the TNA, and is complementary to a
CC portion of the first primer. The first two primers are hybridised to the
CC TNA, and a fused amplification product is created from the TNA using
CC these two primers. The fused product is dissociated, and hybridised to
CC the third primer, which is then extended. The extended modified
CC amplification product is hybridised to the first two primers, and these
CC two primers are ligated. Each of the primers may be labelled using a
CC different label so that the method can be used to detect the presence of
CC a mutation or allele by detecting whether the labelled primer is
CC contained within the fused amplification product or the extended
CC amplification product. The method of the invention combines certain
CC aspects of ligase chain reaction (LCR) and polymerase chain reaction
CC (PCR), but is improved compared to LCR due to the reduced number of
CC primers needed, and the fact that the entire TNA sequence does not need
CC to be known
XX
SQ Sequence 2726 BP; 818 A; 538 C; 642 G; 728 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 2; Length 2726;
XX Best Local Similarity 100.0%; Pred. NO. 0.081;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GCTTGTGATCCAGCAGACTCTCTAC 25
XX |||||
DB 534 GCTTGTGATCCAGCAGACTCTCTAC 510
XX
RESULT 7
ABV78146/c
ID ABV78146 standard; DNA; 3840 BP.
XX
AC ABV78146;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human mdr-1 DNA SEQ ID NO 30.
XX
XX RNA inhibition; dsRNAi; gene expression inhibitor; oncogene; cytostatic;
KM virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-BP000152.
XX
XX 09-JAN-2001; 2001DE-01000586.
XX 26-OCT-2001; 2001DE-01055280.
XX 29-NOV-2001; 2001DE-01058411.
XX 07-DEC-2001; 2001DE-01060151.
XX

XX (RIBO-) RIBOPHARMA AG.
PA Kreutzer R, Limmer S, Rost S, Hadwiger P;
PI WPI; 2002-590671/63.
XX
XX Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
XX Claim 10; Page 131-132; 203pp; German.
XX
XX The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNAi) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNAi is complementary to (I) and at least one end of dsRNAi
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants, introducing an overhang into
CC dsRNAi greatly increases effectiveness for inhibiting gene expression.
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 6; Length 3840;
XX Best Local Similarity 100.0%; Pred. NO. 0.083;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GCTTGTGATCCAGCAGACTCTCTAC 25
XX |||||
DB 2027 GCTTGTGATCCAGCAGACTCTCTAC 2003
XX
RESULT 8
ABZ35722/c
ID ABZ35722 standard; DNA; 3840 BP.
XX
AC ABZ35722;
XX
DT 07-FEB-2003 (first entry)
XX
DE Human mdr-1 polynucleotide SEQ ID NO 30.
XX
XX Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;
KM protozoacide; gene expression; antisense; tumour; infection; plasmodium;
KM virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;
KM Hepatitis C virus; human papilloma virus; gene; ds.
XX
OS Homo sapiens.
XX
PN DE10100588-A1.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2001; 2001DE-01000586.
XX
PR 09-JAN-2001; 2001DE-01000588.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-683450/74.
XX
XX Inhibiting expression of target gene, useful e.g. for treating tumors,
PT by introducing into cells two double-stranded RNAs that are complementary
PT to the target.
XX
PS Claim 13; Page 27-28; 100pp; German.

XX The invention relates to inhibiting expression of a target gene in a cell
CC by introducing at least two oligonucleotides (dsRNA and II), both
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide
CC pairs. At least one of one strand (S1, S2) of the ds structures in each
CC of dsRNA and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumours
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
XX

SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCACGACACTCTTAC 25
DB 2027 GCTTGTGATCCACGACACTCTTAC 2003

RESULT 9
ABX09965/c
ID ABX09965 standard; DNA; 3840 BP.
XX
AC ABX09965;
XX
DT 23-JAN-2003 (first entry)
XX
DE Human mdr-1 DNA fragment SEQ ID 30.
XX
XX Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
KM prion; inhibition; human; ds.
XX
XX Homo sapiens.
OS
PN DE10100587-Cl.
XX
XX 21-NOV-2002.
XX
XX 09-JAN-2001; 2001DE-01000587.
XX
XX 09-JAN-2001; 2001DE-01000587.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
XX Kreutzler R, Limmer S, Rost S, Hadwiger P;
XX WPI; 2002-742209/81.
XX
XX Inhibiting expression of target genes, e.g. oncogenes, in cells, by
XX introduction of complementary double-stranded oligoribonucleotide, after
XX treating the cell with interferon.
XX
XX Disclosure; Page 32-33; 98pp; German.
XX
XX This invention describes a novel method for inhibiting expression of a
XX target gene by introducing into the cell that contains the target gene at
XX least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
XX structure of not more than 49 consecutive nucleotides (nt), where at
XX least a segment of one strand of the ds structure is complementary with
XX the target gene and the cells are treated with interferon before
XX introduction of dsRNA. The method is used to inhibit expression of
XX target genes, particularly oncogenes, cytokine genes, Id (not defined)
XX protein genes; developmental or prion genes, or genes expressed in
XX pathogenic organisms (particularly plasmodia) or in viruses or viroids
XX (pathogenic in humans, animals or plants). Treating the cells with

CC interferon greatly increases the extent to which dsRNA can inhibit
CC expression of the target genes, and the effect is even greater when dsRNA
CC are modified to increase their stability. ABX09936-ABX10075 represent
CC gene fragments used to illustrate the method of the invention
XX

SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCACGACACTCTTAC 25
DB 2027 GCTTGTGATCCACGACACTCTTAC 2003

RESULT 10
ABL91687/c
ID ABL91687 standard; DNA; 3840 BP.
XX
AC ABL91687;
XX
DT 28-MAY-2002 (first entry)
XX
XX Human polynucleotide SEQ ID NO 30.
XX
DE Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KM Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KM cyostatic; virucide; protozoacide; antibacterial; ds.
XX
XX Homo sapiens.
OS
PN DE10100586-Cl.
XX
XX 11-APR-2002.
XX
XX 09-JAN-2001; 2001DE-01000586.
XX
XX 09-JAN-2001; 2001DE-01000586.
XX
XX (RIBO-) RIBOPHARMA AG.
XX
XX Kreutzler R, Limmer S, Rost S, Hadwiger P;
XX WPI; 2002-270454/32.
XX
XX Inhibiting gene expression in cells, useful for e.g. treating tumors, by
XX introducing double-stranded complementary oligoRNA having unpaired
XX terminal bases.
XX
XX Claim 13; Page 28-30; 104pp; German.
XX
XX The invention relates to a method for inhibiting expression of a target
XX gene (ABL91658-ABL91797) in a cell by introducing at least one
XX oligoribonucleotide that has a double-stranded structure consisting of at
XX most 49 sequential nucleotide pairs, with at least one end a single-
XX complementary with the target gene and has at least one end a single-
XX stranded segment of 1-4 nt. The method provides oligoribonucleotides for
XX antisense inhibition of gene expression useful e.g. for treating tumours
XX but the oligoribonucleotides may also be directed against genes present
XX in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans,
XX animals or plants) or against cytokine, Id, developmental or prion genes.
XX The method provides more effective inhibition of gene expression than use
XX of known oligonucleotides, probably because the unpaired overhang
XX increases stability and thus intracellular concentration
XX

SQ Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 3840;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTGTGATCCACGACACTCTTAC 25

```

Db      2027 GCTTGTGATCCACGACACTCTCTAC 2003
      |||||
RESULT 11
ABQ78185/c
ID      ABQ78185 standard; cDNA; 3843 BP.
XX
AC      ABQ78185;
XX
DT      15-NOV-2002 (first entry)
XX
DE      Human MDR1 encoding cDNA SEQ ID NO 1.
XX
KW      Human; immunosuppressant; tacrolimus; cyclosporin; MDR1; SNP;
KW      single nucleotide polymorphism; gene; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..3843
FT              /*tag= a
FT              /product= "MDR1"
FT      variation /replace(2677,A/T)
FT              /*tag= b
FT              /standard_name= "Single nucleotide polymorphism"
XX
PN      JP2002223769-A.
XX
PD      13-AUG-2002.
XX
PF      31-JAN-2001; 2001JP-00024723.
XX
PR      31-JAN-2001; 2001JP-00024723.
XX
PA      (SRLS-) SRL KK.
XX
DR      WPI; 2002-639348/69.
XX      P-PSDB; ABB83950.
XX
PT      Presuming the side effect of an immunosuppressant comprises using a
PT      primer set.
XX
PS      Disclosure; Page 6-11; 14pp; Japanese.
XX
CC      The invention relates to presumption of the side effect of at least one
CC      immunosuppressant selected from tacrolimus and cyclosporin in which if
CC      the 2677th base in the position of MDR1 gene in the encoding region of
CC      the cDNA sequence is guanine, adenine or thymine, is investigated. The
CC      method is used for the presumption of the side effect of an
CC      immunosuppressant. The present sequence is that of the MDR1 encoding cDNA
CC      of the invention
XX
SQ      Sequence 3843 BP; 1129 A; 740 C; 956 G; 1018 T; 0 U; 0 Other;
XX
Query Match      100.0%; Score 25; DB 6; Length 3843;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCTTGTGATCCACGACACTCTCTAC 25
      |||||
Db      2030 GCTTGTGATCCACGACACTCTCTAC 2006
      |||||
RESULT 12
AAZ49332/c
ID      AAZ49332 standard; cDNA; 3860 BP.
XX
AC      AAZ49332;
XX
DT      14-MAR-2000 (first entry)
XX
DE      Human wild-type multidrug resistance-1 (MDR-1) cDNA.

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XX      Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;
KW      hematopoietic stem cell; transplantation; bone marrow transplantation;
KW      chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;
KW      genetic defect; thalassemia; Gaucher's disease; sickle cell anemia;
KW      leukemia; ex vivo expansion; cytokine; wild-type; ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..3843
FT              /*tag= a
FT              /product= "Human wild-type MDR-1 protein"
FT      mutation /replace(553..555, GTT)
FT              /*tag= b
FT              /note= "cDNA sequence of G185V human mutant MDR-1 given
FT              in AAZ49333"
XX
PN      M09961589-A2.
XX
PD      02-DEC-1999.
XX
PF      27-MAY-1999; 99WC-US011825.
XX
PR      28-MAY-1998; 98US-0086988P.
XX
PA      (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PT      Sorrentino B, Bunting K;
XX
DR      WPI; 2000-072615/06.
XX      P-PSDB; AAY58186.
XX
PT      Ex vivo expansion of hematopoietic stem cells transduced with a sequence
PT      encoding human multidrug resistance-1, used for bone marrow
PT      transplantation.
XX
PS      Claim 10; Page 68-70; 113pp; English.
XX
CC      This sequence represents cDNA encoding human wild-type multidrug
CC      resistance protein MDR-1. MDR-1 is a transmembrane efflux pump,
CC      responsible for the export of drugs from cells, particularly cancer
CC      cells. Wild-type MDR-1 shows increased resistance to ecoposide and
CC      decreased resistance to vinca alkaloids compared with a mutant form
CC      (AA58187) where the Gly at position 185 is replaced by Val. The
CC      invention relates to transducing hematopoietic stem cells with nucleic
CC      acid encoding an MDR protein and culturing the modified cells. The
CC      modified haematopoietic stem cells are useful in bone marrow
CC      transplantation (to reconstitute haematopoietic systems in patients who
CC      have undergone chemotherapy or radiation therapy) and in ex vivo gene
CC      therapy of genetic defects in cells derived from haematopoietic stem
CC      cells, e.g., thalassemia, Gaucher's disease, sickle cell anemia or
CC      leukemia. The modified cells can also be used to identify factors
CC      involved in regulating proliferation and differentiation in
CC      haematopoietic stem cells. Haematopoietic stem cells that express MDR-1
CC      will be protected against chemotherapeutic agents, so can be engrafted
CC      while the patient is undergoing chemotherapy. Expansion of (rare)
CC      hematopoietic stem cells provides sufficient cells to permit standard
CC      biochemical analysis. Overexpression of MDR-1 allows cytokine-driven
CC      expansion of haematopoietic stem cells by at least 10-fold compared with
CC      a maximum of 4-fold in known procedures
XX
SQ      Sequence 3860 BP; 1135 A; 746 C; 957 G; 1022 T; 0 U; 0 Other;
XX
Query Match      100.0%; Score 25; DB 3; Length 3860;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCTTGTGATCCACGACACTCTCTAC 25
      |||||
Db      2030 GCTTGTGATCCACGACACTCTCTAC 2006
      |||||

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RESULT 13
AAZ49333/C
ID AAZ49333 standard; cDNA; 3860 BP.
XX
AC AAZ49333;
XX
DT 14-MAR-2000 (first entry)
XX
DE Human G185V mutant multidrug resistance-1 (MDR-1) cDNA.
XX
KM Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;
KM haematopoietic stem cell; transplantation; bone marrow transplantation;
KM chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;
KM genetic defect; thalassemia; Gaucher's disease; sickle cell anaemia;
KM leukaemia; ex vivo expansion; cytokine; mutant; ds.
XX
OS Synthetic.
XX
FH Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3843
FT /tag= a
FT /product= "Human G185V mutant MDR-1 protein"
XX
XX MO9961589-A2.
XX
XX 02-DEC-1999.
XX
XX 27-MAY-1999; 99WO-US011825.
XX
XX 28-MAY-1998; 98US-0086988P.
XX
XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX Sorrentino B, Bunting K;
XX WPI; 2000-072615/06.
XX DR P-PSDB; AAY58187.
XX
XX Ex vivo expansion of haematopoietic stem cells transduced with a sequence
XX encoding human multidrug resistance-1, used for bone marrow
XX transplantation.
XX
XX Example 1; Page 79-82; 113pp; English.
XX
XX This sequence represents cDNA encoding human G185V mutant multidrug
XX resistance protein MDR-1, where the Gly residue at position 185 of the
XX wild-type protein (AAY58186) is replaced by Val. MDR-1 is a transmembrane
XX efflux pump, responsible for the export of drugs from cells, particularly
XX cancer cells. The wild-type MDR-1 shows increased resistance to etoposide
XX and decreased resistance to vinca alkaloids compared with the G185V
XX mutant. The invention relates to transducing haematopoietic stem cells
XX with nucleic acid encoding an MDR protein and culturing the modified
XX cells. The modified haematopoietic stem cells are useful in bone marrow
XX transplantation (to reconstitute haematopoietic systems in patients who
XX have undergone chemotherapy or radiation therapy) and in ex vivo gene
XX therapy of genetic defects in cells derived from haematopoietic stem
XX cells, e.g. thalassemia, Gaucher's disease, sickle cell anaemia or
XX leukaemia. The modified cells can also be used to identify factors
XX involved in regulating proliferation and differentiation in
XX haematopoietic stem cells. Haematopoietic stem cells that express MDR-1
XX will be protected against chemotherapeutic agents, so can be engrafted
XX while the patient is undergoing chemotherapy. Expansion of (rare)
XX haematopoietic stem cells provides sufficient cells to permit standard
XX biochemical analysis. Overexpression of MDR-1 allows cytokine-driven
XX expansion of haematopoietic stem cells by at least 10-fold compared with
XX a maximum of 4-fold in known procedures
XX
XX Sequence 3860 BP; 1135 A; 746 C; 956 G; 1023 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 3; Length 3860;
XX Best Local Similarity 100.0%; Pred. No. 0.083;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 GCTTGTGATCCACGACACTCTTAC 25
DB 2030 GCTTGTGATCCACGACACTCTTAC 2006
XX
XX RESULT 14
XX ABA94365/C
XX ID ABA94365 standard; DNA; 3860 BP.
XX
XX AC ABA94365;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Human BCRP DNA related seq id No. 1.
XX
XX Stem cell; ATP transport protein; ATP-binding cassette; antiparkinsonian;
XX hepatocytic; neurodegenerative; cytostatic; antianemic; muscular; BCRP;
XX cardiac; gene therapy; ds.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT CDS 1..3843
XX FT /tag= a
XX
XX MO200192877-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US017459.
XX
XX 31-MAY-2000; 2000US-00584586.
XX PR 29-MAY-2001; 2001US-00868686.
XX
XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
XX Sorrentino B, Schuetz J;
XX WPI; 2002-114368/15.
XX DR P-PSDB; ABB07266.
XX
XX Identifying a stem cell, for treating e.g., muscular dystrophy,
XX myocardial infarction, Parkinson's disease, or neurodegenerative
XX disorders, comprises detecting the expression of an ATP transport protein
XX (BCRP) by a cell.
XX
XX Disclosure; Page 53-55; 87pp; English.
XX
XX The invention provides a method of identifying and/or isolating a stem
XX cell that involves detecting the expression of an ATP transport protein
XX containing a conserved ATP-binding cassette (BCRP) by a cell in a sample
XX comprising stem cells. The isolated stem cells may be used in the
XX treatment of diseases such as muscular dystrophy, degenerative liver
XX disorder, myocardial infarction, Parkinson's disease, degenerative
XX disorders of the brain, and for tissue regeneration or replacement.
XX Haematopoietic cells can be used in bone marrow transplants (e.g., for
XX treatment of leukemia) and for ex vivo gene therapy for treating blood
XX diseases such as sickle cell anemia and thalassemia. The stem cells can
XX also be used as cell targets in gene therapy protocols. The present
XX sequence represents a sequence related to the BCRP for which no relevant
XX information has been provided in the specification
XX
XX Sequence 3860 BP; 1135 A; 746 C; 957 G; 1022 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 6; Length 3860;
XX Best Local Similarity 100.0%; Pred. No. 0.083;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCTTGTGATCCACGACACTCTTAC 25
XX DB 2030 GCTTGTGATCCACGACACTCTTAC 2006

```

RESULT 15

ABA94366/C

ID ABA94366 standard; DNA; 3860 BP.

XX ABA94366;

XX 26-MAR-2002 (first entry)

XX Human BCRP DNA related seq Id No. 3.

XX Stem cell; ATP transport protein; ATP-binding cassette; antiparkinsonian;
 XX hepatocytic; neurodegenerative; cytosolic; antianemic; muscular; BCRP;
 KM cardiac; gene therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT CDS 1..3843
 XX FT /*tag= a

XX WO200192877-A2.

XX 06-DEC-2001.

XX 30-MAY-2001; 2001WO-US017459.

XX 31-MAY-2000; 2000US-00584586.

XX 29-MAY-2001; 2001US-00866866.

XX (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX Sorrentino B, Schuetz J;

XX WPI; 2002-114368/15.

XX P-PSDB; ABB07267.

PT Identifying a stem cell, for treating e.g., muscular dystrophy,
 PT myocardial infarction, Parkinson's disease, or neurodegenerative
 PT disorders, comprises detecting the expression of an ATP transport protein
 PT (BCRP) by a cell.

XX Disclosure; Page 59-60; 87pp; English.

XX The invention provides a method of identifying and/or isolating a stem
 CC cell that involves detecting the expression of an ATP transport protein
 CC containing a conserved ATP-binding cassette (BCRP) by a cell in a sample
 CC comprising stem cells. The isolated stem cells may be used in the
 CC treatment of diseases such as muscular dystrophy, degenerative liver
 CC disorder, myocardial infarction, Parkinson's disease, degenerative
 CC disorders of the brain, and for tissue regeneration or replacement.
 CC Haematopoietic cells can be used in bone marrow transplants (e.g., for
 CC treatment of leukemia) and for ex vivo gene therapy for treating blood
 CC diseases such as sickle cell anemia and thalassemia. The stem cells can
 CC also be used as cell targets in gene therapy protocols. The present
 CC sequence represents a sequence related to the BCRP for which no relevant
 CC information has been provided in the specification

XX SQ Sequence 3860 BP; 1135 A; 746 C; 956 G; 1023 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 25; DB 6; Length 3860;

XX Best Local Similarity 100.0%; Pred. No. 0.083;

XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTGTGATCCACGACACTCTCTAC 25

Db 2030 GCTTGTGATCCACGACACTCTCTAC 2006

Search completed: February 9, 2005, 16:05:59
 Job time : 245.69 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 13:42:02 ; Search time 2448.85 Seconds
(without alignments)
388.593 Million cell updates/sec

Title: US-10-007-255-15

Perfect score: 25 gcttgatccacgacactcctac 25

Sequence: 1 gcttgatccacgacactcctac 25

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapex 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 66479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_hlc.*
- 4: gb_est3.*
- 5: gb_est4.*
- 6: gb_est5.*
- 7: gb_est6.*
- 8: gb_g981.*
- 9: gb_g982.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	568	5	BP243819 BP243819
2	25	100.0	579	5	BP242809 BP242809
3	25	100.0	3843	9	AY408954 Homo sapi
4	25	100.0	3843	9	AY408955 Pan trogl
5	22	88.0	497	5	BX645450 DKFZp781C
6	20.8	83.2	534	4	BM414475 EST01407
7	20.8	83.2	569	5	BX317766 BX317766
8	20.8	83.2	574	5	BX320207 BX320207
9	20.8	83.2	588	6	CA058097 ssalngae51
10	20.8	83.2	592	6	CA044923 ssalngae00
11	20.8	83.2	595	5	BX310867 BX310867
12	20.8	83.2	619	5	BX868539 BX868539
13	20.8	83.2	623	6	CA052009 ssalngae53
14	20.8	83.2	627	6	CR369095 CR369095
15	20.8	83.2	642	6	CB507124 ssalob505
16	20.8	83.2	658	6	BX317788 BX317788
17	20.8	83.2	691	6	CA040401 ssalhc50
18	20.8	83.2	701	7	CR375818 CR375818
19	20.8	83.2	729	6	CA055205 ssalngae54
20	20.8	83.2	747	5	BX875171 BX875171
21	20.8	83.2	755	5	BX871907 BX871907
22	20.8	83.2	773	5	BX884053 BX884053
23	20.8	83.2	773	5	BX884541 BX884541
24	20.8	83.2	782	5	BX320208 BX320208

25	20.8	83.2	792	5	BX861388	BX861388
26	20.2	80.8	688	5	BU478361	BU478361
27	20.2	80.8	726	6	BH704692 BOMG53TF	BH704692
28	19.2	76.8	547	5	BX874038	BX874038
29	19.2	76.8	682	6	CR509048	CR509048
30	19.2	76.8	728	7	CR362263	CR362263
31	19.2	76.8	912	9	CL208918	CL208918
32	18.8	75.2	641	4	BJ699561	BJ699561
33	18.8	75.2	645	4	BJ676814	BJ676814
34	18.8	75.2	650	4	BJ533210	BJ533210
35	18.8	75.2	650	4	BJ700611	BJ700611
36	18.8	75.2	661	1	AU091247	AU091247
37	18.8	75.2	661	4	BJ014564	BJ014564
38	18.8	75.2	764	4	BJ505685	BJ505685
39	18.8	75.2	786	4	BJ720789	BJ720789
40	18.8	75.2	830	7	CN986052	CN986052
41	18.8	75.2	853	7	CN986052	CN986052
42	18.8	75.2	854	7	CN986052	CN986052
43	18.8	75.2	856	7	CN977721	CN977721
44	18.8	75.2	858	7	CN987415	CN987415
45	18.8	75.2	1011	4	BJ740383	BJ740383

ALIGNMENTS

RESULT 1
BP243819/c 568 bp mRNA linear EST 15-SEP-2004
LOCUS BP243819 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone
DEFINITION HEP21483, mRNA sequence.
ACCESSION BP243819
VERSION BP243819.1 GI:52116729
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., China,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL Contact: Yutaka Suzuki
COMMENT Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source location/Qualifiers
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/mol_type="mRNA"
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/clone="HEP21483"
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/note="hepatoma"

ORIGIN
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Best Local Similarity 100.0%; Pred.No. 0.56; Indels 0;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;

OY 1 GCTTGTGATCCACGACACTCCTAC 25
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DB 546 GCTTGTGATCCACGACACTCCTAC 522
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RESULT 2
BP242809/c 579 bp mRNA linear EST 15-SEP-2004
LOCUS BP242809

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DEFINITION      BP242809 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone
                  HEP17994, mRNA sequence.
ACCESSION       BP242809
VERSION         BP242809.1  GI:52115719
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS         Mzushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE           Sequence comparison of human and mouse genes reveals a homologous
                block structure in the promoter regions
JOURNAL         Genome Res. 14 (9), 1711-1718 (2004)
COMMENT         Contact: Yutaka Suzuki
                Department of Virology
                Institute of Medical Science, University of Tokyo
                4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                Email: yusuzuki@ims.u-tokyo.ac.jp.
                Location/Qualifiers
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source          /organism="Homo sapiens"
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                /db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.56;
Matches          25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              1 GCTTGTGATCCAGCAGCACTCTCTAC 25
Db              252 GCTTGTGATCCAGCAGCACTCTCTAC 228
RESULT 3
LOCUS           AY408954/c 3843 bp DNA linear GSS 15-DEC-2003
DEFINITION      Homo sapiens ABCB1 gene, VIRUTAL TRANSCRIPT, partial sequence,
ACCESSION       AY408954
VERSION         AY408954.1  GI:39764922
KEYWORDS        GSS.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 3843)
AUTHORS         Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
                Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sniensky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE           Inferring nonneutral evolution from human-chimp-mouse orthologous
                gene trios
JOURNAL         Science 302 (5652), 1960-1963 (2003)
COMMENT         2 (bases 1 to 3843)
                Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
                Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
                Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sniensky,J.J.,
                Adams,M.D. and Cargill,M.
TITLE           Direct Submission
                Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                Rockville, MD 20850, USA
                This sequence was made by sequencing genomic exons and ordering
                them based on alignment.
                Location/Qualifiers
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QY              1 GCTTGTGATCCAGCAGCACTCTCTAC 25
Db              2030 GCTTGTGATCCAGCAGCACTCTCTAC 2006
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DEFINITION      DKFZP781C1343.r1.781 (synonym: h1cc4) Homo sapiens cDNA clone
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                Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.63;
Matches          25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              1 GCTTGTGATCCAGCAGCACTCTCTAC 25
Db              2030 GCTTGTGATCCAGCAGCACTCTCTAC 2006
RESULT 5
LOCUS           BX645450/c 497 bp mRNA linear EST 04-SEP-2003
DEFINITION      DKFZP781C1343.r1.781 (synonym: h1cc4) Homo sapiens cDNA clone
                DKFZP781C1343.5', mRNA sequence.
                Location/Qualifiers
FEATURES

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ACCESSION BX645450
VERSION BX645450.1 GI:34479783
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 497)
AUTHORS Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weill, B., Amid, C., Oeanger, A., Fodor, G., Han, M. and Wiemann, S.
TITLE EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
 MIPS
 Ingolsteedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert
 clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center,
 Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 81 sequence available.
 This clone (DKFZp781C1343) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 Location/Qualifiers
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 /lab_host="DH10B"
 /clone_lib="781 (synonym: hlcc4)"
 /note="Vector: pSPORT1_Sfi; Site_1: SfiI; Site_2: SfiI; cDNA-collection"
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 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GCTTGTGATCCAGCAGACTCC 22
 22 GCTTGTGATCCAGCAGACTCC 1
RESULT 6
 BM414475 534 bp mRNA linear EST 01-JAN-2004
LOCUS EST01407 Atlantic salmon lambda Zap Express ovary cDNA library
DEFINITION Salmo salar cDNA clone oyr_004_d08 5', mRNA sequence.
ACCESSION BM414475
VERSION BM414475.1 GI:40542222
KEYWORDS EST.
SOURCE Salmo salar (Atlantic salmon)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE 1 (bases 1 to 534)
AUTHORS Caplice, N.C., Martin, S.A., Davey, G.C. and Powell, R.
TITLE An expressed sequence tag-based list of genes expressed in the testis and ovary of Atlantic salmon (Salmo salar)
JOURNAL Unpublished (2002)
COMMENT Contact: Caplice NC
 Department of Microbiology
 National University of Ireland Galway (NUIG)
 National University of Ireland Galway, Galway, Ireland
 Tel: 00353 91 524411 2254
 Fax: 00353 91 525700

Email: nicole.caplice@nuiagalway.ie
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 High quality sequence scop: 535
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 /note="Organ: ovary; Vector: lambda Zap Express; Site 1: EcoRI; Site 2: XhoI; An Atlantic salmon ovary cDNA library was constructed using the lambda Zap Express/Gigapack cloning kit (Stratagene cloning systems). cDNA synthesis was carried out using an oligo (dT) primer for the reverse transcription of 5ug of mRNA and the library was constructed by directional cloning EcoRI-XhoI based on manufacturers instructions. An insert:vector ligation ratio of 1:5 was chosen as most optimum. The lambda library was packaged with Gigapack III gold packaging extracts and plated on the E. coli cell line XL1-Blue MRF."
ORIGIN
 Query Match 83.2%; Score 20.8; DB 4; Length 534;
 Best Local Similarity 91.7%; Pred. No. 56;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 2 CTTGTGATCCAGCAGACTCTAC 25
 356 CTTGTGATCCAGCAGACTCTAC 333
RESULT 7
 BX317766 569 bp mRNA linear EST 14-MAY-2004
LOCUS BX317766 tcay Oncorhynchus mykiss cDNA clone tcay0033b.p.22 3pr.im,
DEFINITION mRNA sequence.
ACCESSION BX317766
VERSION BX317766.2 GI:40308402
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 569)
AUTHORS Govoroun, M., Guiguen, Y. and Le Gac, F.
TITLE Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss
JOURNAL Unpublished (2003)
COMMENT On Apr 7, 2003 this sequence version replaced gi:29598411.
 Contact: Guiguen Y
 INRA - SCRIBE
 Campus de Beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenastupport@jouy.inra.fr to obtain the chromatogram of this sequence.
 Plate: 0033 row: p column: 22
 Seq primer: M13F.
FEATURES
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 Location/Qualifiers
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/lab_host="DH10B"
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/notes="Vector: pT73D-pac; Rainbow trout multi-tissues -
normalized + 1 subtraction (tcay); Clone distribution :
AGENAS Resource centre, Francois Plumi,
Francois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (IREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Query Match      83.2%; Score 20.8; DB 5; Length 569;
Best Local Similarity 91.7%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CTTGTGATCCAGGACACTCTCTAC 25
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Db      385 CTTGTGATCCAGGACACTCTCTAC 362

RESULT 8
BX320207/c      574 bp      mRNA      linear      EST 20-MAY-2004
LOCUS      BX320207 tcay Oncorhynchus mykiss cDNA clone tcay0038b.a.22 3prtm,
DEFINITION      mRNA sequence.
ACCESSION      BX320207
VERSION      BX320207.2 GI:40309605
KEYWORDS      EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
ORGANISM      Oncorhynchus mykiss
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
            1 (bases 1 to 574)
            Govoroun,M., Guiguen,Y. and le Gac,F.
            Construction and primary characterization of normalized cDNA
            libraries in rainbow trout, Oncorhynchus mykiss
            Unpublished (2003)
            On Apr 7, 2003 this sequence version replaced gi:29600852.
            Contact: Guiguen Y
            INRA - SCRIBE
            Campus de Beaulieu, RENNES cedex, 35042, France
            Tel: 02.23.48.50.09
            Fax: 02.23.48.50.20
            Email: Yann.Guiguen@beaulieu.rennes.inra.fr
            Sequence cleaned of vector, adaptor and repetitions. Contact us
            at eigenasupport@jouy.inra.fr to obtain the chromatogram of this
            sequence.
            Plate: 0038 row: a column: 22
            Seq primer: M13F.

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            AGENAS Resource centre, Francois Plumi,
            Francois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et

```

```

Etude du genome (IREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Query Match      83.2%; Score 20.8; DB 5; Length 574;
Best Local Similarity 91.7%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      328 CTTGTGATCCAGGACACTCTCTAC 305

RESULT 9
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LOCUS      CA058097
DEFINITION      ssalrge513143 mixed_tissue Salmo salar cDNA, mRNA sequence.
ACCESSION      CA058097
VERSION      CA058097.1 GI:24388340
KEYWORDS      EST.
SOURCE      Salmo salar (Atlantic salmon)
ORGANISM      Salmo salar
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
            1 (bases 1 to 568)
            GRASP Consortium, Davidson,W.S., Koop,B.F. and
            http://web.uvic.ca/cbr/grasp.
            A survey of Salmo salar transcripts from high complexity cDNA
            libraries
            Unpublished (2002)
            Contact: Koop BF
            Centre for Biomedical Research
            University of Victoria
            PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
            Tel: 250 472 4067
            Fax: 250 472 4075
            Email: bkoop@uvic.ca
            Genome Sciences Centre, BC Cancer Agency
            cDNA preparation, sequencing and bioinformatics:
            Y Butterfield, R Kirkpatrick, J Asano, N Gilm, R Guin, D Lee,
            S Lee, T Olson, P Pandoh, A Prabhu, D Smalls, L Spence, J Scott,
            S Taylor, G Yang, J Schein, S Jones and M Marra.

FEATURES
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            Genetics; Atlantic salmon tissue contributors: Carlo
            Biagi, Mitch Un and Robert Devlin (DFO, Vancouver, B.C.),
            Simon Jones (PBS, Nanaimo, B.C.), Seasprixy Hatchery
            (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN
Query Match      83.2%; Score 20.8; DB 6; Length 588;
Best Local Similarity 91.7%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CTTGTGATCCAGGACACTCTCTAC 25
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RESULT 10
CA044923      592 bp      mRNA      linear      EST 04-MAR-2003
LOCUS      CA044923
DEFINITION      ssalrge003036 gut Salmo salar cDNA, mRNA sequence.
ACCESSION      CA044923
VERSION      CA044923.1 GI:24349786

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KEYWORDS	EST.
SOURCE	Salmo salar (Atlantic salmon)
ORGANISM	Salmo salar
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
AUTHORS	1 (bases 1 to 592) GASP Consortium, Davidson, W. S., Koop, B. F. and http://web.uvic.ca/cbr/grasp.
TITLE	A survey of Salmo salar transcripts from high complexity cDNA libraries Unpublished (2002)
JOURNAL	Contact: Koop BF Centre for Biomedical Research University of Victoria PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada Tel: 250 472 4067 Fax: 250 472 4075 Email: bkoop@uvic.ca
COMMENT	Centre for Biomedical Research, University of Victoria cDNA preparation and sequencing: Roberto Alberto, Marianne Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop. bioinformatics: Gordon D Brown.
FEATURES	Location/Qualifiers 1..592 /organism="Salmo salar" /mol_type="mRNA" /strategy="McConnell" /db_xref="taxon:8030" /clone_id="gut" /note="Vector: pBluescriptISK; Library Creator: Matthew L Rise; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seespring Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)."
ORIGIN	
Query Match	83.2%; Score 20.8; DB 6; Length 592;
Best Local Similarity	91.7%; Pred. No. 56;
Matches	22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB	
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LOCUS	BX910867 cdk Oncorhynchus mykiss cDNA clone tcbk0072c.m.23 5prim,
DEFINITION	mRNA sequence.
ACCESSION	BX910867
VERSION	BX910867.2 GI:43415782
KEYWORDS	EST.
SOURCE	Oncorhynchus mykiss (rainbow trout)
ORGANISM	Oncorhynchus mykiss Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE	1 (bases 1 to 595) Govoroun, M., Guiguen, Y. and Le Gac, F. Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss Unpublished (2003)
AUTHORS	On Jan 22, 2004 this sequence version replaced gi:41127666. Contact: Guiguen Y
TITLE	INRA - SCRIE
JOURNAL	Campus de Beaulieu, RENNES cedex, 35042, France
COMMENT	Tel: 02.23.48.50.09 Fax: 02.23.48.50.20 Email: Yann.Guiguen@beaulieu.rennes.inra.fr

```

Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0072 row: m column: 23
Seq primer: M13R.
Location/Qualifiers
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/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_id="tcba"
/notes="Vector: pT73D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution: AGENAE Resource centre. Francois PIUMI,
Francois.PIUMI@jouy.inra.fr, INRA, CRA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

```

/note="Vector: pT73D-pac; Rainbow trout multi-tissues - normalized + 1 subtraction; Clone distribution : AGENAE Resource centre, Francois Piumi, Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

LOCUS CR369095 642 bp mRNA linear EST 21-APR-2004
DEFINITION CR369095 AGENAE Rainbow trout normalized testis library (tcbl)
ACCESSION Oncorhynchus mykiss cDNA clone tcbl0021c.n.22 5prim, mRNA sequence.
CR369095
VERSION CR369095.1 GI:46480407
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

Query Match 83.2%; Score 20.8; DB 5; Length 619;
Best Local Similarity 91.7%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

REFERENCE Govoroun, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cDNA libraries in rainbow trout, *Oncorhynchus mykiss*
Unpublished (2003)
CONTACT: Guiguen Y

QY 2 CTTGTGATCCAGGACACTCTCTAC 25
Db 619 CTTGTGATCCAGGATCACTCTCTAC 596

JOURNAL

COMMENT

RESULT 13
CA052009 623 bp mRNA linear EST 04-MAR-2003
LOCUS ssalrghb31310 mixed_tissue Salmo salar cDNA, mRNA sequence.
DEFINITION CA052009
ACCESSION CA052009.1 GI:24382252
VERSION EST.
KEYWORDS Salmo salar (Atlantic salmon)
SOURCE Salmo salar
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

FEATURES

source location/Qualifiers

REFERENCE 1 (bases 1 to 623)
AUTHORS GRASP Consortium, Davidson, W.S., Koop, B.F. and
TITLE http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA libraries

JOURNAL Unpublished (2002)
COMMENT Contact: Koop BF

FEATURES

1..642 location/Qualifiers
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcbl0021c.n.22"
/tissue_type="testis"
/lab_host="RDH10B"
/clone_lib="AGENAE Rainbow trout normalized testis library (tcbl)"

Genome Sciences Centre, BC Cancer Agency
cDNA preparation, sequencing and bioinformatics:
Y Butterfield, R Kirkpatrick, J Asano, N Ginn, R Guin, D Lee,
S Lee, T Olson, P Pandoh, A Prabh, D Smalhus, L Spence, J Stott,
S Taylor, G Yang, J Schein, S Jones and M Marra.
Location/Qualifiers

Query Match 83.2%; Score 20.8; DB 7; Length 642;
Best Local Similarity 91.7%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES
source 1..623

/organism="Salmo salar"
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/clone_lib="mixed_tissue"
/note="Vector: pCWSport6; Library Creator: Research Genetics; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seagrang Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"

RESULT 15
CB507124 657 bp mRNA linear EST 16-MAY-2003
LOCUS ssalob50534 reproductive Salmo salar cDNA, mRNA sequence.
DEFINITION CB507124
ACCESSION CB507124.1 GI:29318770
VERSION EST.
KEYWORDS

ORIGIN

SOURCE Salmo salar (Atlantic salmon)

Query Match 83.2%; Score 20.8; DB 6; Length 623;
Best Local Similarity 91.7%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

JOURNAL

COMMENT

QY 2 CTTGTGATCCAGGACACTCTCTAC 25
Db 598 CTTGTGATCCAGGATCACTCTCTAC 581

JOURNAL

COMMENT

RESULT 14
CR369095/c

COMMENT

Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: brcorp@vic.ca
Genome Sciences Centre, BC Cancer Agency CDNA preparation,
sequencing and bioinformatics: Y Butterfield, R Kirkpatrick, J
Amano, N Guin, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D
Smalhus, L Spence, J Scott, S Taylor, G Yang, J Schein, S Jones and
M Marra.

POLYMER

FEATURES

Source

Location/Qualifiers
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Kristian R von Schalburg; Atlantic salmon tissue
contributors: Carlo Biagi, Mitch Un and Robert Devlin
(DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.),
Seaspring Hatchery (Crofton, B.C.), Rachel Roper
(University of Victoria)"

ORIGIN

Query Match 83.2%; Score 20.8; DB 6; Length 657;

Best Local Similarity 91.7%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTTGTGATCCAGGACACTCTAC 25
|||||
Db 433 CTTGTGATCCAGGATACCTCTAC 456

Search completed: February 9, 2005, 21:55:48
Job time : 2451.85 secs

